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#### STIC-Biotech/ChemLib

| Searcher: _ |      |  |
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| Phone:      | <br> |  |
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Location:

Clerical: \_\_\_\_ Online time: \_

Date Picked Up: 1/3/1/9

Date Completed 38
Searcher Prep/Review:

STIC-ILL

Wednesday, July 31, 2002 6:32 AM STIC-Biotech/ChemLib FW: RE: 10/006,163

Imp rtance: High

Request for you.

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From:

Sent: To:

Subject:

-----Original Message-----

From: Huynh, Phuong N.

Sent: Tuesday, July 30, 2002 6:03 PM

To: STIC-ILL Subject: RE: 10/006,163

Imp rtance: High

- 1. Please search polypeptide of SE SEQ NO: 1 (open) against commercial and interference database.
- 2. Also please do oligopeptide search of SEQ ID NO: 1 against commercial and interference database.

Thanks, Neon Art unit 1644 Mail 9E12 Tel 308-4844

Edward Hart Technicai Info. Specialist STIC/Biotech CMI 6B02 Tel: 305-9203

| TYPE OF SEARCH: | VENDOR/COST (where applic.) |
|-----------------|-----------------------------|
| NA Sequences:   | STN:                        |
| AA Sequences:   | DIALOG:                     |
| Structures:     | Questel/Orbit:              |
| Bibliographic:  | DRLink:                     |
| Litigation:     | Lexis/Nexis:                |
| Full text:      | Sequence Sys.:              |
| Patent Family:  | WWW/Internet:               |
| Other:          | Other (specify):            |

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Minimum
Maximum
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Perfect score:
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Maximum Match 100%
Listing first 45 summaries
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Copyright (c) 1993 - 2000 Com
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|---|--|------------|---|
|   | RESULT 1 US-09-019-216-1 US-09-019-216-1 Sequence 1, App Patent No. 598 GENERAL INFORM APPLICANT: APPLICANT: APPLICANT: ITILE OF INV NUMBER OF SE CORRESPONDEN ADDRESSEE: CORFUTER: COUNTRY: ZIP: 942 COMPUTER REF COMPUTER REF COMPUTER REF COMPUTER REP MEDIUM TY: COMPUTER REP MEDIUM TY: COMPUTER REP MEDIUM TY: COMPUTER: OPERATING SOFTWARE: CURRENT APPLICATION FILING DAN CLASSIFICATION FILING DAN CLASSIFICATION FILING DAN CLASSIFICATION FILING DAN CLASSIFICATION FILING DAN INTELEPHONE INAMEL BAI REGISTRATI REFERENCE FELECOMMUNIC TELEPHONE TELEPHONE TELEPHONE TELEPHONE TYPE: ami STRANDEDNE TYPE: ami STRANDEDNE LIBRARY: LIBRARY: LIBRARY: LIBRARY: SUS-09-019-216-1  | •          | 28 158. 29 157. 30 157. 31 155. 32 155. 33 152. 36 144. 37 141. 41 16. 42 136. 43 13.   |
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|   | /09019216  I C. MAN SHORT CHAIN DEHYDROGENASE  armaceuticals, Inc. Dr.  Dr.  Dr.  Dr.  Dr.  Dr.  Dr.  Dr   | ALIGNMENTS | US-08-457-245-5. US-08-822-322-9 US-09-466-109-9 US-09-468-738A-29 US-08-440-856A-4 5229279-7 US-09-002-298-6 US-09-002-298-7 US-09-002-298-7 US-09-002-298-7 US-07-637-865-2 US-08-858-207A-270 US-09-109-205-1 US-09-109-25-1 US-08-762-129-4 US-08-762-129-4 US-08-762-129-1 US-08-762-129-1 US-08-762-129-1 US-08-762-129-1 US-08-762-129-1 US-09-468-738A-2  |
|   | SE .   |            | Sequence 5, Appli<br>Sequence 9, Appli<br>Sequence 9, Appli<br>Sequence 29, Appli<br>Sequence 4, Appli<br>Patent No. 5229279<br>Sequence 6, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 7, Appli<br>Sequence 270, Appli<br>Sequence 270, Appli<br>Sequence 270, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 4, Appli<br>Sequence 2, Appli<br>Sequence 2, Appli<br>Sequence 4, Appli<br>Sequence 2, Appli |

Query Match Best Local Similarity

100.0%;

Score 1623; DB 2; Pred. No. 2.8e-183;

Length 313;

DB 2;

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US-09-019-216-3
                                                                                                                                                                                  ATTORNEY AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-855-0555
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
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                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOPTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
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                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RPLICANT: Lal, Preeti
RPLICANT: Corley, Neil C.
RITLE OF INVENTION: HOMAN SHORT CHAIN DEHYDROGENASE
      LIBRARY: Genucian Cone: 2315796
                                                 TOPOLOGY: line
MMEDIATE SOURCE:
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                                                                               TYPE: amino acid
STRANDEDNESS: sir
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US-08-594-808B-7
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Best Local Similarity
                               TELEX: 620420
INFORMATION FOR SEQ ID NO: 7
SEQUENCE CHARACTERISTICS:
SEQUENCE CASE amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             quence 7, Application US/08594808B
tent No. 5804423
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,
                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: (718) 884-6600
                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           296 MGKEEVAKYIPPQIKLPKWVIWQSVNRF
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                                                                                                                                                                                                                                                                                                                                                                                              STREET: 5676
CITY: Bronx
                                                                                                     TELEFAX:
                                                                                                                                                       REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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10471-0900
                            amino acid
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                                                                                                         718/601-1099
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protein
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Pred. No. 5e-64;
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181 ARMSTDMAVELNPYNVCVVTLIPGPVKTETANRTIIDDAYKMIKENPELEE----FIKGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      61 ITSRGGKGIALYYDHSNWTEVKFLFEKIKEDEEGKLDILVNNVYNSLGKATEMIGKTFFD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 51 AQSLGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWE 110
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                                                                                                                                                                                                                                                                                     DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM---AKEEVLQDPVLKQFKSAFSSAE
                                                                                                                STEYTGKALARLAMDPGKLKKSGKTLFTEDLAQKYDFSDKHGAGMEPQNIRSIRTILG-T
                                                                                                                                                                       TTELSGKCVVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPV--QDYLSLSSVLSHV
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA: APPLICANT: Sahm, Hermann
APPLICANT: Hollenberg, Cornelles P
TITLE OF INVENTION: MICROBIOLOGICAL METHOD
TITLE OF INVENTION: 5-KETOGLUCONATE
NUMBER OF SEQUENCES: 7 APPLICATION NUMBER: US/08/594,808B Bringer-Meyer, Stephanie of Karl F. Ross, g OF MAKING

US-08-594-808B-7

Matches Query Match

66;

Conservative

32;

Indels

21; Gaps

5

256;

Score 222.5; DB 1 Pred. No. 8.9e-18; Mismatches

Local Similarity

5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64

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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                             FILING DATE: 20-JUL-1994 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE
                                                                                                                                                                                                               FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
                                                                                                                      TELEPHONE: 713.787.1400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         175 ATDWGRHGLQINGLAPGYFATEMTERLVADEE 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       121 NAVFFVGQAVARHMIPRGRGKIVNICSVQSELARPGI-----APYTATKGAVKNLTKGM 174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         125 RGHYFCSYYGARLMYPAGQGLIVVISS-----PGSLQYMFNVPYGYGKAACDKLAADC 177
                                                                                                                                                                                                                                                                                                                                                          FILING DATE: 2
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC
OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              69 VTDQDAVIDGVAAIERD-MGPIDILINN--AGIQ-----RRAPLEEFSRKDWDDLMSTNV 120
                                                                                                                                                                           NAME: Kammerer, Patricia A. REGISTRATION NUMBER: 29,775
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     65 SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL 124
      STRANDEDNESS:
                                                                                                                                                            REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CITY: Houston
                                                                                                                                                                                                                                                          APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB 9414622.2
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                      amino acid
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                                      315 amino acids
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Fentem, Phillip A
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US-08-793-035-10
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Best Local S
Matches 75
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                NFORMATION FOR SEQ ID NO: 10:
                                                                                                                                                 PRIOR APPLICATION NUMBER: GB95,
APPLICATION NUMBER: GB95,
APPLICATION TATE: 17-UII-1995
                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Relicurrent Application Data: Application NUMBER: US,
                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
SEQUENCE CHARACTERISTICS
                                                                  TELECOMMUNICATION INFORMATION:
                                                                                                                                       ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                 PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     238
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 236 VVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        179 HELRRHGVSCVSLWPGIVQTEL---LKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           178 IDLNLTGVFLCTQAATKIMMKKRKGRIINIASVVGLIGNIGQANYAAAKAGVIGFSKTAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           120 NNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCA 178
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                126 TFGGDVSKEADVEAMMKTA-IDAWGTIDVVVNN--AGI-----TRDTLLIRMKKSQWDEV 177
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   66 AVPKVESPVVVVTGASRGIGKAIALSIGKAGCKVLVNYARSAKEAEEVSKQIEAYGGQAI 125
                                                                                                      REGISTRATION NUMBER: 29,779
                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY: US
ZIP: 77210-4433
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: TX
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                                                TELEPHONE:
                                                                                     REFERENCE/DOCKET NUMBER:
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                                                                                     MOBT: 132
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Pred. No. 1.3e-1
0; Mismatches 1
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; STRANDEDNESS: s1; TOPOLOGY: linear US-08-793-035-10

Length 315;

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Best Local Similarity
""" hes 72; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; TYPE: PRT ; ORGANISM: Staphylococcus aureus US-09-238-481-2
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CURRENT FILING DATE: 1999-01-28
RUMBER OF SEQ ID NOS: 2
SOFTWARE: FastSEQ for Windows Version 3.0
SEQ ID NO 2
LENGTH: 246
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Patent No. 6110704
GENERAL INFORMATION:
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APPLICANT: McDevitt, Damien
TITLE OF INVENTION: FabG
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                                   240
                                                                     174 SRGITVNAVAPGFIVSDMTDALSDEL-KEQMLTQIPLARFGQD;DIANT---
                                                                                                      183 RHGVSCVSLWPGIV---QTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVAL 239
                                                                                                                                                                           130 CSVYGARLMVPAGQGLIVVISS-----PGSLQYMFNVPYGVGKAACDKLAADCAHELR 182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity
les 75; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              66 AVPKVESPVVVVTGASRGIGKAIALSLGKAGCKVLVNYARSAKEAEEVSKQIEAYGGQAI 125
                                                                                                                                                                                                                   8
                                                                                                                                                                                                                                               70 EVRTLEEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGHYF 129
                                                                                                                                                                                                                                                                                                                      11 VVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCVPVVCDSSQES 69
                                                                                                                                                                                                                                                                                    8 LYTGASRGIGRSIALQLAEEGYNVAVNYAGSKEKAEAVVEEIKAKGVDSFAIQANVADAD 67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG 287
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IDLNLTGVFLCTQAATKIMMKKRKGRIINIASVVGLIGNIGQANYAAAKAGVIGFSKTAA 237.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAP-MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCV 59
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGASRNINVNVVCPGFIASDMTAKLGEDMEK-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCA 178
                                   ATD 242
                                                                                                                                          CIQKATPQMLRQRSGAIINLSSVVGAVGNPGQANYV-----ATKAGVIGLTKSAARELA
                                                                                                                                                                                                             EVKAMIKEV-VSQFGSLDVLVNN--AGI----TRDNLLMRMKEQEWDDVIDTNLKGVFN 119
                                                                                                                                                                                                                                                                                                                                                         13.2%;
nilarity 29.6%;
Conservative 3
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                                                                                                                                                                                                                                                                                                                                                         36;
                                                                                                                                                                                                                                                                                                                                                                        Score 214.5; DB 3; Pred. No. 7.3e-17;
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RESULT 8 US-09-466-109-8

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RESULT 7
US-08-822-322-8
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US-08-822-322-8
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Matches
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/822,322
FILING DATE: 21-March-1997
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TELECOMMUNICATION INFORMATION:
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APPLICATION NUMBER: DE 196
FILING DATE: 21-March-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: ami
222 DIAYICV
                                       230 ELSGKCV 236
                                                                                                                    171 DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSS-AETT 229
                                                                                                                                                                                              119 INNVGLRGHYFCSVYGARLMVPAGQGLIVV-----ISSPGSLQYMFNVPYGVGKAAC 170
                                                                                168 KSAALDCA--LKDYDVRVNTVHPGYIKTPLVDDLPGAEEAMS----QRTKTPMGHIAEPN
                                                                                                                                                           110 LLAVNLDGVFFGTRLGIQRMKNKGLGASIINMSSIEGFVGDPSLGAY--NASKGAVRIMS
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                                                                                                                                                                                                                                                                         59 VPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDD 118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OPERATING SYSTEM:
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                                                                                                                                                                                                                                        58 QFFQHDSSDEDGWTKLFDATEK-AFGPVSTLVNNAGIAV-----NKSVEETTTAEWRK 109
                                                                                                                                                                                                                                                                                                                                                                                                                      Local
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                                                                                                                                                                                                                                                                                                                                           1 MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLG--GQC
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Alcohol dehydrogenase and its use for
enzymatic production of chiral hydroxy compounds
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RESULT 9
US-08-440-856A-3
; Sequence 3, Application US/08440856A
; Patent No. 5750873
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Best Local S
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GENERAL RICCHOL BETTINE
GENERAL BETTINE
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MEDIUM TYPE: Diskette, 3.5 inch, 360 kb storage
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ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
CITY: New York City
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                                                                                                                                                                                                                                                                        DIAYICV 228
                                                                                                                                                                                                                                                                                                                                                  ELSGKCV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                 KSAALDCA--LKDYDVRVNTVHPGYIKTPLVDDLPGAEEAMS----QRTKTPMGHIAEPN 221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSS-AETT 229
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   QFFQHDSSDEDGWTKLFDATEK-AFGPVSTLVNNAGIAV-----NKSVEETTTAEWRK 109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDD 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MSNRLDGKVAIITGGTLGIGLAIATKFVEEGAKVMITGRHSD---VGEKAAKSVGTPDQI 57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLG--GQC 58
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             71; Conservative
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OPERATING SYSTEM: PC-DOS
SOFTWARE: Wordperfect
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 252 amino acids
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28.7%;
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Pred. No. 1.2e-14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches 105;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         BOER 1076
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                                                      US-09-413-814-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Query Match
Best Local S
Sequence 9, Application US/09413814
Patent No. 6225064
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   OPERATING SYSTEM: PC-D
SOFTWARE: PatentIn Rel
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 337 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION: TELEPHONE: (202) 887-1517
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQUENCES: 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
                                                                                                                                                            198
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                                                                                                                         278 VEKMEEVVRGLATLKGPTLRPRDIAEAVLFLASDEARYISGHNLVVDGGVTTSRNLIGL 336
                                                                                                                                                                                                                             174 AADCAHELRRHG--VSCVS-----LW-----
                                                                                                                                                                                                                                                                                                                                                                        55
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: MILLMAN, ROBERT A REGISTRATION NUMBER: 36, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/0 FILING DATE: 15-MAY-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY: U
ZIP: 20037
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: MORRISON & FOERSTER
                                                                        10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYI-----TGRHLDTLRVVAQEAQSL 54
                                                                                                                                                                                                                                                                                                                                                                                                   MPKRLDGKVAIVTGGARGIGEAIVRLFAKHGARVVIADIDDAAGEAL------ASAL 99
                                                                                                                                                          TELLKEHMAKEEVLQDPVLKQFKSA-----FSSAETTELSGKCVV----ALATDPNILSL 248
                                                                                                                                                                                               TKNAACELRAHGVRVNCVSPFGVATPMLINAWROGHDDATADADRDLDLDUDVTVPSDQE 277
                                                                                                                                                                                                                                                                  EFDRVLRVNALGAALGMKHAARAMAPRRAGSIVSVASVAAVLGGLGPHAYTASKHAIVGL 217
                                                                                                                                                                                                                                                                                                   MWDDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGS-LQYMFNVPYGVGKAACDKL 173
                                                                                                                                                                                                                                                                                                                                   GPQVSFVRCDVSVEDDVRRAVDWALSRHGGRLDVYCNN--AGVLGRQTRAARSILSFDAA 157
                                                                                                                                                                                                                                                                                                                                                                        GGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPAS 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WASHINGTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DELLAPORTA, STEPHEN L.

VENTION: MATERIALS AND METHODS FOR PRODUCING

VENTION: PLANTS WITH SINGLE-SEX FLOWERS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (202) 887-0763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              11.5%;
llarity 27.4%;
Conservative 3
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linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PENNSYLVANIA AVE. N.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US/08/440,856A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 186; Db 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 123;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 337;
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                                                                                                                                                                                                                                 ----- 197 197
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9

APPLICANT: Gesellschaft fuer Biotechnologische Forschung APPLICANT: Bristol-Myers Squibb, Co.

APPLICANT: APPLICANT:

Bloecker, Helmut Brandt, Petra Cino, Paul M

Beyer, Stefan Bristol-Myers Squibb,

APPLICANT: Dougherty, Brian APPLICANT: Goldberg, Steven

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Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                          SEQ ID NO 2
LENGTH: 257
TYPE: PRT
ORGANISM: Rhodobacter sphaeroides
S-09-287-097-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 2, Application US/09287097 Patent No. 6255093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches 69;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
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CURRENT FILING DATE: 1999-10-07
EARLIER APPLICATION NUMBER: DE 198 46 493.2
EARLIER FILING DATE: 1998-10-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 31
TYPE: PRT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      EARLIER APPLICATION NUMBER: DE/19815685.5 EARLIER FILING DATE: 1997-04-08
                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQ ID NOS: 2
SOFTWARE: PatentIn Ver.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CURRENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: RECOMBINANT MICROBIAL 3-HYDROXYBUTYRATE DEHYDROGENASE. TITLE OF INVENTION: A PROCESS FOR ITS PRODUCTION AND THE USE THEREOF FILE REFERENCE: 1614-9007
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ITLE OF INVENTION: DNA sequences for enzymatic synthesis of polyketide or ITLE OF INVENTION: heteropolyketide compounds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: SCHMUCK, Rainer
APPLICANT: MULLER, Rainer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PPLICANT: KRUGER, Kerstin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PPLICANT: ENGEL, Alfred
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PPLICANT: WEISSER, Harald
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     202 AAYSIAKTGVLILTRSLATEEAPHGILVNCVS--PGLIDNGYLPPAQKEWMER 252
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    162 -PYGVGKAACDKLAADCAHELRRHG--VSCVSLWPGIVQTELL----KEHMAK 207
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          146 LAAMTDDEWRNVMDSNLSSV----HYLCRAAVARMRQRKSGRIINIGLSPTYAIRGAPNV 201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             112 PASMWDD------INNVGLRGHYFCSVYGARL-MVPAGQGLIVVISSPGSLQYMFNV 161
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       98 RALGRRTMVVQADVTRPNAAAELESSVE-AQLGPIDILVNNV------GDFFFKP 145
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    52 QSLGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWET 111 :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: | :: 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              2 AAP-----MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEA 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/09/287,097 FILING DATE: 1999-04-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Reichenbach,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Mueller, Joachim
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hofle,
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            Conservative
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            36;
                                                         Pred.
                                                     Score 178.5;
Pred. No. 1.
            Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .2e-13;
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                                                                                      DB 4;
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                                                                                      Length
            Indels
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            39;
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Patent No. 6143538
                                                                                                                                      Matches
                                                                                                                                                                       Query Match
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                                                                                                                                                                                                                                                                                                                                               TELEFAX: 630-252-2779
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 40486
REFERENCE/DOCKET NUMBER: S-
TELECOMMUNICATION INFORMATION:
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MEDIUM TYPE: FLOPPY DISK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                         TOPOLOGY: 1: MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                            SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          169
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           121 NVGLRGHYFCSVYGARLMVPAGQGLIV-VISSPGSLQYMFNVPYGVGKAACDKLAADCAH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       223 ATTGQIGGTVV 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61 IAADMSDGEACRALIETA-----GGCDILVNN--AGIQHV-----SSIEEFPVGKWNAIL 108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             61 VVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDIN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTATION SYSTEM: MS-105
COPTWARE: WORDPERFECT 6.22
                                                                    13
                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/026,4828 FILING DATE: 02/19/98
 73
                              65 SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL 124
                                                                                                                                                        Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE:
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                                                                                                                                                                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                RELEPHONE:
                                                                                               5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AETTELSGKCV 236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ETAGKGITCNAICPGYVLTPLVEAQIPDQMKAHDMDRETVIREVMLDRQPSRQF-----
LTDMNAIDQLSQQI-MASVDHVDFLINNAGRSIRRAVHESFDRFHDFERTM----
                                                                    VKGKVALITGASSGIGLTIAKRIAAAGAHVLLVARTQETLEEVKAAIEQQGGQASIFPCD
                                                                                                                                                      n 10.9%;
Similarity · 24.4%;
                                                                                                                                                                                                                                                                                           amino acid
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                                                                                                                                                                                                                                                                                                                                                                630-252-27
                                                                                                                                      Conservative
                                                                                                                                                                                                                                                       ss: single
linear
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                                                                                                                                                                                                                                                                                                             amino acids
                                                                                                                                                                                                                                         protein
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                                                                                                                                      48;
                                                                                                                                                                                                                                                                                                                                                                                                                    S-87814
                                                                                                                                      Score 176.5; DB 4;
Pred: No. 3.1e-12;
B; Mismatches 115;
                                                                                                                                        Indels
                                                                                                                                                                       Length 295;
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                                                                                                                                           Query Match
Best Local
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                                                                                                                                                                                                                                                                                                                                                                                          TELEFAX: (212) 838-381 (NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,962B
FILING DATE: 20-January-1995
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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APPLICATION NUMBER:
FILING DATE: 6-Octob
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ITLE OF INVENTION:
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                                                                                                                                                                                                                            NAME/KEY:
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                    67
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Pasqualini, Patricia A.
REGISTRATION NUMBER: 34,894
REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OPERATING SYSTEM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STREET:
                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
STRANDEDNESS: si
                                                                                                                                                                                                                                                                                                                                                                                                                             TELEPHONE:
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                                                                                                                                           Local Similarity
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                                                                                                                                                                                                                                                                                                                                                       ENGTH:
GKIALVTGASRGIGRAIAETLAARGGKVIGTATSENGAQAI---SDYLGANGKGLMLNVT 61
                                                                                    GOVCVVTGASRGIGRGIALOLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCDSS 66
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCV 236
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T: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New York
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VENTION: Isolated Nucleic Acid Molecule

VENTION: Mich Codes for A 32 kDa Protein Having 11-CIS Retinol

VENTION: Dehydrogenase Activity, and Which Associates With P63,

VENTION: a Portion of a Retinol Binding Protein Receptor
                                                                                                                                                                                                                                                                                                                                                    244 amino acids
                                                                                                                         Conservative
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                                                                                                                                                                                                                            E.coli 3-oxoacyl[acyl carrier protein]
reductase (FABG)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IBM
                                                                                                                                                                                                                                                                                                      linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    6-October-1994
                                                                                                                                                                                                                                                                                   protein
                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                         838-3884
                                                                                                                                        10.5%;
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                                                                                                                         45;
                                                                                                                                         Score 171; DB 1; Length 244; Pred. No. 1e-11;
                                                                                                                       'Mismatches 111; Indels 30;
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                                                                                                                                                                                          ; NAME/KEY: E.coli 3.oxoacyl[acyl carrier protein]reductase
; NAME/KEY:
US-08-562-114B-13
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                                                                                                              Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO:
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TITLE OF INVENTION:
TITLE OF INVENTION:
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      OPERATING SYSTEM: PC-DOS
SOFTWARE: WORDPEFFECT 5.1 and ASCII
CURRENT APPLICATION DATA:
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APPLICATION NUMBER:
FILING DATE: 20-Janu
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                                                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                                         MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STATE: NC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     174 ITVNVVAPGFIETDMTRALSDDQRAGILAQVPAGRLGGAQEIANAVAFLASDEAAYITGE 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       186
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  114 VFRLSKAVMRAVMKKRHGRITTIGSVVGTMGNGGQANYAAAKAGLIGFSKSLAREVASRG 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: FILING DATE: 22-NO. CLASSIFICATION: 435
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TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                         NAME: Kohli, Vineet REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER:
                                                                                                                                                                                                                                                                                        TYPE: amino acid
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                                                                              GQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCDSS 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     VSCVSLWPGIVQTEL - - - LKEHMAKEEVLQDPV - - -
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                                             GKIALVTGASRGIGRAIAETLAARGGKVIGTATSENGAQAI---SDYLGANGKGLMLNVT 61
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1: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New York
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24.4%;
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                                                                                                                          Score 171; DB 2
Pred. No. 1e-11;
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 244 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SOFTWARE: Wordperfect CURRENT APPLICATION DATA:
                                                                                                                                                  MOLECULE TYPE: protein
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                                                                                                                                                                                                                                                                                                                   REGISTRATION NUMBER: 30,946
                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: 08/375, ye FILING DATE: 20-January-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/729,594A FILING DATE: 11-October-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     62
                                                                                                                  NAME/KEY: E.coli 3-oxoacyl[acyl carrier protein]reductase
                                                                                                                                                                                                                                                                                                        REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
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5. 6280997
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New York City
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                 10.5%; Score 171; DB 4
24.4%; Pred. No. 1e-11;
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                                                                                                 VSCVSLWPGIVQTEL - - - LKEHMAKEEVLQDPV - - -
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Search completed: July 31, 2002, 15:09:36 Job time: 125 sec

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Run on:
                                                                   OM protein - protein search, using sw model
July 31, 2002, 15:12:06 ; Search time 17.45 Seconds (without alignments)
1723.551 Million cell updates/sec
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Title: Perfect score: Sequence: Scoring table: 1 MAAPMNGQVCVVTGASRGIG......YLPSFLRVPKWIIALYTSKF 313 US-10-006-163-1 313

OLIGO Gapop 60.0 , Gapext 60.0

Searched: 283138 seqs, 96089334 residues

Word size :

0

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters:

283138

Post-processing: Listing first 45 summaries

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Database : PIR\_71:\* pir2:\*
pir3:\*
pir4:\* pirl:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| 29                                       | ) k                | ) C    | 2 2    | 24     | 23     | 22                 | 21     | 20                 | 19                 | 18     | 17                 | 16     | 15      | 14     | 13     | 12     | 11      | 10     | ω       | 00       | 7        | 6      | u        | 4        | ω       | N      | μ      | :  | Result     |
|--|--------------------|--------|--------|--------|--------|--------------------|--------|--------------------|--------------------|--------|--------------------|--------|---------|--------|--------|--------|---------|--------|---------|----------|----------|--------|----------|----------|---------|--------|--------|--|------------|
| ωv                                       | o u                | o ve   |        | 10     | 10     | 10                 | 10     | 10                 | 10                 | 10     | 10                 | 10     | 10      | 10     | 10     | 10     | 10      | 10     | 10      | 10       | 10       | 10     | 10       | .10      | 10      | 11     | 16     | Score  |            |
| 2.9                                      |                    |        |        |        | ٠      |                    |        | ٠                  | ٠                  | ٠      |                    |        |         |        |        |        |         |        |         |          |          |        |          | •        | 3.2     | ٠      | 5.1    | Match  | %<br>Query |
| 245                                      | 244                | 241    | 240    | 521    | 339    | 325                | 302    | 293                | 286                | 271    | 262                | 254    | 249     | 248    | . 246  | 246    | 246     | 245    | 244     | 244      | 244      | 244    | 244      | 244      | 244     | 251    | 323    | Length   |            |
| N  |                    |        |        |        |        |                    |        |                    |                    |        |                    |        |         |        |        |        |         |        |         |          |          |        |          |          | بر      | N      | N      | B  |            |
| B97491                                   | 106063             | CBSISS | H75014 | C87474 | AE2212 | T29604             | T44578 | AE1927             | G83378             | S34678 | E70604             | G75333 | S05398  | G83253 | в89896 | C83961 | A69621  | B83462 | AD0642  | AB0195   | C85672   | T44434 | T12051   | G90812   | B42147  | H2     | T32125 | Ħ  |            |
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| short chain dehydr<br>hypothetical prote | probable short cha | short- | 1-[ac  |        |        | hypothetical prote |        | 3-ketoacyl-acyl ca | probable short-cha |        | hypothetical prote | Ω.     | in poly | short- | 7      | l-(acy | l-(acyl | short- | l-[acyl | 1-(acyl- | 1-[acyl- | -      | 1-[acyl- | 1-[acyl- | 1-[acy] | 1-[acy | otheti | ription  |            |

| .45                | 44                | 43                   | 42                 | 41                 | 40                 | 39                 | 38                 | 37                 | 36     | 35                 | 34                 | 33                 | 32                 | 31                 | 30                 |  |
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| 80                 | œ                 | 9                    | 9                  | 9                  | ب                  | 9                  | 9                  | 9                  | ø      | ø                  | 9                  | 9                  | 9                  | 9                  | 9                  |  |
| 2.6                | 2.6               | 2.9                  | 2.9                | 2.9                | 2.9                | 2.9                | 2.9                | 2.9                | 2.9    | 2.9                | 2.9                | 2.9                | 2<br>9             | 2.9                | 2.9                |  |
| 177                | 173               | 320                  | 285                | 274                | 266                | 257                | 256                | 255                | 251    | 248                | 248                | 248                | 247                | 247.               | 247                |  |
| ν                  | N                 | N                    | N                  | N                  | 2                  | N                  | _                  | N                  | N      | N                  | N                  | N                  | N                  | N                  | N                  |  |
| 139709             | AD3517            | S22450               | G87298 .           | G83284             | F83127             | AE3190             | A57149             | AC3438             | AI2708 | E81026             | F81971             | F82128             | T12020             | F82776             | S77280             |  |
| fixR homolog - Agr | probable carbonyl | · 3-oxoacyl-[acyl-ca | short chain dehydr | probable short-cha | probable short-cha | 3-oxoacyl-(acyl-ca | gluconate 5-dehydr | ribitol-5-phosphat |        | 3-oxoacyl-(acyl-ca | probable 3-oxoacyl | 3-oxoacyl-(acyl-ca | 3-oxoacyl-(acyl-ca | 3-oxoacyl-[ACP] re | 3-oxoacyl-[acyl-ca |  |

## ALIGNMENTS

| C;Genetics: A;Gene: CESP:F59E11.2 A;Map position: 5 A;Introns: 20/1; 60/1; 108 Query Match  | A; Molecule type: DNA<br>A; Residues: 1-323 <bra><br/>A; Cross-references: EMBL:A<br/>A; Experimental source: str</bra>   | <pre>submitted to the EMBL Data Library, July 199/ A;Description: The sequence of C. elegans cosmid F5 A;Reference number: Z21124 A;Accession: T32125 A;Status: preliminary; translated from GB/EMBL/DDBJ</pre> | nypothetical protein F59E11.2 - C:Species: Caenorhabditis elegans C:Date: 29-Oct-1999 #sequence_rev C:Accession: T32125 R:Bradshaw, H.   | RESULT 1<br>T32125 |
|---|---|---|--|--------------------|
| C;Generics:<br>C;Generics:<br>A;Gene: CESP::F59E11.2<br>A;Map position: 5<br>A;Introns: 20/1; 60/1; 108/3; 135/2; 166/2; 192/3; 227/3; 280/1<br>Query Match 5.1%; Score 16; DB 2; Length 323; | A;Molecule type: DNA<br>A;Residues: 1-323 <bra><br/>A;Cross-references: EMBL:AF016685; PIDN:AAB66216.1; GSPDB:GN00023; CESP:F59E11.2<br/>A;Experimental source: strain Bristol N2; clone F59E11</bra> | Submitted to the MML Data Library, July 1997 A;Description: The sequence of C. elegans cosmid F59E11. A;Reference number: Z21124 A;Recession: T32125 A;Status: preliminary; translated from GB/EMBL/DDBJ        | nypothetical protein FyBil.2 - Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Species: Caenorhabditis elegans C;Acces: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 29-Oct-1999 C;Accession: T32125 C;Accession: T32125 |                    |

밁 Best Local Similarity 100 Matches 16; Conservative 100.0%; Pred. No. 1.7e-08; tive 0; Mismatches 0; Indels 0 Gaps

0

3-oxoacyl-{acyl-carrier protein] reductase [imported] - Anabaena sp. (strain PCC 71; C;Species: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Date: 14-Dec-2001 #sequence\_revision 14-Dec-2001 #text\_change 11-Jan-2002

Accession: AH2042

R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriq Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabai DNA. Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840
A;Accession: AH2042

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-251 <KUR>

A;Cross-references: GB:BA000019; PIDN:BAB73593.1; PID:g17130984; GSPDB:GN00179 A;Experimental source: strain PCC 7120

C; Genetics:

A;Gene: fabG C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

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A;Accesson. C. DNA
A;Accesson. C. DNA
A;Aclecule type: DNA
A;Residues: 1-42,'R','44-45 <VER>
A;Residues: 1-42,'R','44-45 <VER>
A;Cross-references: GB:M87040; NID:g145885; PIDN:AAA23743.1; PA;Cross-references: GB:M87040; PIDN:AAA23743.1; PIDN:AAA23
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          J. Biol. Chem. 267, 5751-5754, 1992
A;Title: The gene encoding Escherichia coli
A;Reference number: A42147; MUID:92210530
A;Molecular
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Pathway: fatty acid biosynthesis
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
C;Keywords: fatty acid biosynthesis; NADP; oxidoreductase
F;6-182/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;6-36;Region: beta-alpha-beta NADP nucleotide-binding fold
F;151/Active site: Tyr #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Molecule type: DNA
A; Residues: 1-29, (G', 31-244 <RAW)
A; Residues: 1-29, (G', 31-244 <RAW)
A; Cross references: GB: M84991; NID: 9145879; PIDN: AAA23739.1; PID: 9145881
A; Cross references: GB: M84991; NID: 9145879; PIDN: AAA23739.1; PID: 9145881
A; Verwoert, I.I.; Verbree, E.C.; van der Linden, K.H.; Nijkamp, H.J.; Stu
J. Bacteriol. 174, 2851-2857, 1992
A; Title: Cloning, nucleotide sequence, and expression of the Escherichia
A; Reference number: A41856; MUID: 92234941
A; Accession: C41856
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Date: 30-Sep-1993 #sequence_revision 31-Oct-1997 C;Accession: B64853; B42147; C41856 R;Blattner, F.R.; Plunkett III, G.; Bloch, C.A.; Pe A.; Rose, D.J.; Mau, B.; Shao, Y. Science 277, 1453-1462, 1997 A;Title: The complete genome sequence of Escherichi A;Reference number: A64720; MUID:97426617
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3-oxoacyl-(acyl-carrier-protein) reductase (EC 1.1.1.100)
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G90812
3-oxoacyl-[acyl-carrier-protein] reductase [imported] -
C;Species: Escherichia coli
C;Date: 18-Jul-2001 #sequence_revision 18-Jul-2001 #text
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C;Species: Escherichia coli
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A; Residues: 1-244 <BI
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                          A; Reference number: 222768
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KHAYASHA, N.; Yasunaga, T.; Kuhara, J.; gasawara, N.; Yasunaga, T.; Kuhara, J.; Kuhara, J.; A; Yasunaga, T.; Kuhara, J.; Kuhara, J.; Yasunaga, T.; Kuhara, J.; Yasunaga, R.; Yasunaga, N.; Yasunaga, T.; Kuhara, J.; Yasunaga, N.; Yasunaga, N.; Yasunaga, N.; Yasunaga, N.; Yasunaga, N.; Yasunaga, N.; Yasunaga, T.; Kuhara, J.; Yasunaga, T.; Kuhara, J.; Yasunaga, N.; Yasunaga, T.; Kuhara, J.; Yasunaga, N.; Yasunaga, T.; Kuhara, J.; Yasunaga, N.; Yasunaga, N.; Yasunaga, N.; Yasunaga, T.; Kuhara, J.; Yasunaga, N.; Yasunaga, N.; Yasunaga, T.; Kuhara, J.; Yasunaga, N.; Yasunaga, N
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A; Molecule type: DNA
A; Residues: 1-244 <HAY>
A; Cross-references: GB:BA000007; PIDN:BAB34894.1;
A; Cross-references: Strain O157:H7, substrain F
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      C;Function:
Activate acid biosynthesis
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
C;Keywords: fatty acid biosynthesis; NADP; oxidoreductase
C;Keywords: short-chain alcohol dehydrogenase homology <SAD>
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C;Date: 16-Jul-1999 #sequence_revision
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C; Superfamily: ribitol dehydrogenase;
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3-oxoacy1-{acy1-carrier-protein} reductase (EC 1.1.1.100) [imported] - Moritella C; Species: Moritella marina C; Species: Moritella marina C; Date: 21-Jan-2000 #sequence_revision 21-Jan-2000 #text_change 04-Mar-2000 C; Accession: T44434 R; Morita, N.; Ueno, A.; Tanaka, M.; Ohgiya, S.; Hoshino, T.; Kawasaki, K.; Yumoto Biotechnol. Lett. 21, 641-646, 1999
A; Title: Cloning and sequencing of clustered genes involved in fatty acid biosynt
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           R; Shen, Z.; Byers, D.M.
J. Bacteriol. 178, 571-573, 1
A; Title: Isolation of Vibrio
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Masunaga, T.;
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source: strain B392
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A;Title: Genome sequence of Yersinia pestis, the causative agent of plague. A;Reference number: AB0001; MUID:21470413; PMID:11586360 A;Accession: AB0195
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C; Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
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C;Keywords: oxidoreductase
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A;Cross-references: EMBL:AB021978; PIDN:BAA85256.1
A;Experimental source: ATCC 15381
C;Genetics:
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A; Residues: 1-244 < KUR>
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A; Residues: 1-244 <STO>
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R; Perna, N.T.; Plun
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).Species: Yersinia pestis
).Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 27-Nov-2001
);Accession: AB0195
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Superfamily: ribitol dehydrogenase; short-chain; Reywords: oxidoreductase
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3-oxoacyl-[acyl-carrier protein] reductase [imported] - Salmonella enterica subsp. (c):Species: Salmonella enterica subsp. enterica serovar Typhi
A;Note: this species has also been called Salmonella typhi
C;Date: 09-Nov-2001 #sequence_revision 09-Nov-2001 #text_change 27-Nov-2001
C;Accession: AD0642
R;Parkhill, J.; Dougan, G.; James, K.D.; Thomson, N.R.; Pickard, D.; Wain, J.; Churc th, T.; Connerton, P.; Cronin, A.; Davis, P.; Davies, R.M.; Dowd, L.; White, N.; Fai
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A; Residues: 1-244 < PAR>
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C; Superfamily:
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C; Superfamily:
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                                                                                                                                                                                         A;Cross-references: GB:AE004576; GB:AE004091; NID:g9947415; PIDN:AAG04859.1; A;Experimental source: strain PAO1
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A; Residues: 1-245 <STO>
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.029;
                                                                                                                                    alcohol dehydrogenase
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A.; Larbig,
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A;Experimental source: Strain 168
C;Genetics:
A;Gene: FabG; srb
A;Map position: 135-145 degrees
C;Function:
A;Description: EC 1.1.1.00 [validated, MUID:96326321].
A;Description: EC 1.1.1.00 [validated, MUID:96326321].
A;Pathway: fatty acid biosynthesis
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Reywords: fatty acid biosynthesis; NADP; oxidoreductase
F;5-185/Domain: short-chain alcohol dehydrogenase homology <SADH>
F;154/Active site: Tyr #status predicted
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C83961
3-oxoacyl-(acyl-carrier protein) reductase fabG [imported] - Bacillus halodurans
C;Species: Bacillus halodurans
C;Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
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A;Residues: 230-246 (OGU)
A;Cross-references: DDBJ:D64116; NID:g1389548; PIDN:BAA10974.1; PID:g1237012
R;Cronan, J.E.; Morbidoni, H.R.; de Mendoza, D.
J. Bacteriol. 178, 4794-4800, 1996
A;Title: Bacillus subtilis acyl carrier protein is encoded in a cluster of la;Reference number: 233107; MUID:96326321
A;Accession: 746633
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C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: A69621; PC4176; T46633
R;Kunst, F; Ogasawara, N; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Berter
C: Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, N.M.; Chd
A; Ehrlich, S.D.; Emmerson, P.T.; Entian, K.D.; Errington, J.; Fabret, C.; Ferrari, E.
Nature 390, 249-256, 1997
Nature 390, 249-256, 1997
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N;Alternate_names: 3-ketoacyl-acyl carrier protein reductase
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Best Local Similarity
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#sequence_revision 01-Dec-2000 #text_change 03-Aug-2001
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0.029;
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                                                                               A;Reference number: A82950; MUID:20437337
A;Accession: G83253
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R; Stover, C.K.; Pham, X.Q.;
R; Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
.; Lory, S.; Olson, M.V.
Nature 406, 959-964, 2000
                                                                                                                                                                                                                                                                                                                                             C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                          A; Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                               probable short-chain dehydrogenase PA3128 [imported] - Pseudomonas aeruginosa
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R;Kuroda, M; Ohta, T; Uchiyama, I; Baba, T; Yuzawa, H; Kobayashi, I; Cui, L; ma, A; Mizutani Ui, Y; Kobayashi, N; Sawano, T; Inoue, R; Kaito, C; Sekimizu, C; Shiba, T; Hattori, M; Ogasawara, N; Hayashi, H; Hiramatsu, K. Lancet 357, 1225-1240, 2001

A;Title: Whole genome sequencing of meticillin-resistant Stapylococcus aureus. A; Reference number: A89758; MUID:21311952; PMID:11418146
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3-oxoacyl-(acyl-carrier protein) reductase [imported] - Staphylococcus aureus C;Species: Staphylococcus aureus C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 22-Oct-2001 C;Accession: B89896
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C; Superfamily: ribitol dehydrogenase;
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A;Molecule type: DNA
A;Residues: 1-246 <KUR>
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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A;Molecule type: DNA
A;Rosidues: 1-246 <STO>
A;Cross-references: GB:AP001515; GB:BA000004; NID:g10174886; PIDN:BAB06210.1; GSPDB:GA;Experimental source: strain C-125
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R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fuji, F.;
Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: C83961
                                                                                                                                                                                                                                                                  A;Cross-references: GB:BA000018; pID:g13701031; pIDN:BAB42326.1; A;Experimental source: strain N315
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Matches 10
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Erwin, A.L.; Mizoguchi, L.L.; Coulter, S.N.; Fo

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Search completed: July 31, 2002, 15:14:17 Job time: 131 sec
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A;Note: gra-orf6
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
C;Keywords: NAD; oxidoreductase
F;9-187/Domain: short-chain alcohol dehydrogenase homology <SADH>
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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A;Experimental source: strain PA01
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; Residues: 1-249 <SHE>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ;Title: Structure and deduced function of the granaticin-producing polyketide synthase;Reference number: S05393; MUID:90060034
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ;Sherman, D.H.; Malpartida, F.; Bibb, M.J.; Kieser, H.M.; Bibb, M.J.; Hopwood, D.A.
MBO J. 8, 2717-2725, 1989
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Molecule type: DNA
Residues: 1-249 <ICH>
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Perfect score:
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Q47202 escherichia
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Q91401 streptomyce
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## ALIGNMENTS

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| 194 GIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALATDDNILSLSGKVL 253 | 134 GARLMYPAGQGLIYYISSPGSLQYMFNYPYGYGKAACDKLAADCAHELRRHGYSCYSLWF 193 | CARI MUDACOCI TIVIT CCDCCI OVACNIJOVOVOVA ACOLI ADOLAGIT DBUCVCOVCI ED | 74 LFEQVDREQQGRLDVLVWNAYAGVQTILNTRNKAFWETPASKWDDINNVGLRGHYFCSVY 133 | 74 LFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASWWDDINNVGLRGHYFCSVY 133 | Matches 240; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | 76.7%; S | SEQUENCE 313 AA; 33909 MW; 832F83FA75D931A3 CRC64; |    | Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases. | "NEDO human cDNA sequencing project."; |     | Irle R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakami B., | Nakagawa K., Mizuno S., Morinaga M., Kawamura M., Suqiyama T., | , Suzuki Y., Hata H | Oshima A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K., | TISSUE-TESTIS; | SEQUENCE FROM N.A. | [1]    | NCBI_TaxID=9606; | Chordata; |   | CDNA FLJ25430 FIS, CLONE TST06262. | (TrEMBLrel. 19, | (TrEMBLrel. 19, | 01-DEC-2001 (TrEMBLrel. 19, Created) |   | O96LJ7 PRELIMINARY: PRT: 313 AA. | 17 1 × |

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HOMO Saplens (Human).
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01-DEC-2001 (TIEMBLIEL. 19, Created)
01-DEC-2001 (TIEMBLIEL. 19, Last sequence update)
01-DEC-2001 (TIEMBLIEL. 19, Last annotation update)
SIMILAR TO RIKEN CONA 1110029G07 GENE.
                                                                                                                                                                                                    SEQUENCE FROM N.A.
TISSUE-PANCREATIC ADENOCARCINOMA;
Strausberg R.;
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Q96B59;
01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
HTPDTHETICAL 33.9 KDA PROTEIN.
HOMO sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Submitted (OCT-2001) to the
EMBL; BC015943; AAH15943.1;
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TISSUE-MELANOMA;
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BC014057; AAH14057.1; -
NCE 313 AA; 33925 MW; 37FA022675C4F076 CRC64;
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Catarrhini; Hominidae;
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RA Aizawa K., Izawa M., Nishi K.; Riyosawa H., Kasukawa T., Saito R.,
RA Saito T., Okazaki Y., Gojobori T., Bono H., Kasukawa T., Saito R.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Fleischmann W., Gaasterland T., Gissi C., King B., Kochiwa H.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
RA Schriml L.M., Statubi F., Suzuki R., Tomita M., Wagner L., Washio T.,
RA Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
RA Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
RA Brownstein M.J., Bult C., Fletcher C., Fujita M., Gariboldi M.,
RA Lyons P., Marchionni L., Mashima J., Mazzarelli J., Mombaerts P.,
RA Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
RA Sasaki H., Sato K., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
Suzuki H., Toyo-oka K., Wang K.H., Weitz C., Whittaker C., Wilming L.,
RA Hayashtzaki Y., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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Best Local S
Matches 39
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EMBL; AK003958; BABE33093.1; --
MGD; MGI:1915960; 1110029607Rik.
SEQUENCE 313 AA; 34031 MW; E
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Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; F
Eukaryota; Metazoa; Chordata; Sciurognathi; Muridae;
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5.6e-3;
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Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea;
Eukaryota; Peloderinae; Caenorhabditis.
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HSSP; P50162; 1AE1.
InterPro; IPR002198; ADH_short.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
                                                               "Direct Submission.";
Submitted (JUL-2001) to
-I- SIMILARITY: BELONGS
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                                                                                                                                 STRAIN-BRISTOL N2;
Holmes A., Elliot G., Cloud
*The sequence of C. elegans
Submitted (MAR-1999) to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE
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Hypothetical
                                                                                                      STRAIN-BRISTOL N2;
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MEDLINE-99069613; PubMed-9851916;
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                                                                                             Waterston
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protein;
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Rodentia;
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01-DCT-2001 (TIEMBLIEL 1
PUTATIVE OXIDOREDUCTASE.
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InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
Hypothetical protein; Oxidoreductase.
SEQUENCE 323 AA; 35824 MW; 4FE24D30ED39CAE3
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Submitted (AUG-2001) to
-1- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consorscience 282:2012-2018(1998).
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Rhabditidae; Pelode:
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Streptomyces coelicolor
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7) to the
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                                                                                                                                                                                                                                                                                                                                                                                                                          CRC64;
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Best Local S
Matches 13
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Matches 13
                                                                            Wang L. Vining L.C.;

"Control of antibiotic biosynthesis and cell differentiation in Streptomyces venezuelae ISP5230 by JadW1, a homolog of the gamma butyrolactone autoregulators BarX and Afsa.";

Submitted (OCT-2001) to the EMBL/GenBank/DDBJ databases.

EMBL; U34659; AALJ3836.1; -.

SEQUENCE 254 AA; 26434 MW; 4347A4FEE372B752 CRC64;
                                                                                                                                                                                    Streptomyces venezuelae.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                                                                 Q934T1 PRELIMINARY;
Q934T1;
01-DEC-2001 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                           STRAIN-ISP5230;
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                                                                                                                                                                                                                                                                                                                                                                                                                   Oxidoreductase.
SEQUENCE 250 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     EMBL; AL359214; CA
HSSP; Q12634; 1YBV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the 8 Mb Streptomyces coelicolor A3(2)
Mol. Microbiol. 21:77-96(1996).
-I- SIMILARITY: BELONGS TO THE SHORT-CI
                                                                                                                                                                                                                                                                                                                                                                                                                                          PRINTS;
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Kinashi H., Hopwood D.A.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro;
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Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces,
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100.0%;
Conservative
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IPR000244; Ribosomal_
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e EMBL/GenBank/DDBJ databases.
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Pred. No.
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Pred. No.
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RESULT
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Best Local S
Matches 10
                                                                                                                                                                                                                                                              STRAIN-MP-1 (ATCC 15381);
Morita N., Ueno A., Tanaka M., Ohgiya S., F
Yumoto I., Ishizaki K., Okuyama H.;
"Cloning and sequencing of clustered genes
biosynthesis from the docosahexaenoic acid-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Q47202;
Q47202;
01-NOV-1996
                                                                                                                                                                                                      Biotechnol. Lett. 21:641
      Oxidoreductase
SEQUENCE 244
                                            PRINTS; PR00080; SDRFAMILY, PROSITE; PS00061; ADH_SHORT
                                                                                        Pfam; PF00106; adh_short
                                                                                                                                       EMBL; AB021978; BAA85256.1; -. HSSP; P19992; 1HDC.
                                                                                                                                                                                                                                                    marinus strain MP-1.
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SEQUENCE
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01-MAY-2000 (TrEMBLrel 13,
01-DEC-2001 (TrEMBLrel 19,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Vibrio marinus (Moritella
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q9RÁ33;
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Stuitje A.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 CBI_TaxID-90736;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               J. Bacteriol. 174:2851-2857(1992).
EMBL; M87040; AAA23743.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE=92234941; PubMed=1314802; Verwoert I.I.G.S., Verbree E.C.,
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01-NOV-1996 (TIEMBLIEL 01, Last sequence update)
01-DEC-2001 (TIEMBLIEL 19, Last annotation update)
MALONYL COENZYME A-ACYL CARRIER PROTEIN (FABD) (FRAGMENT).
                                                                                                                    nterPro;
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                                                                                                               IPR002198; ADH_short
      244 AA;
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                                         ADH_SHORT;
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25558 MW; 871DD5CF7B7F00E3 CRC64;
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19, Last annotation update)
PROTEIN] REDUCTASE HOMOLOG.
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Pred. No.
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y bacterium,
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Matches 10
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Matches
SEQUENCE FROM N.A.

STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

STRAIN-ATCC 15692 / PAO1;

STOVER C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrene Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lag Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yug Garber R.L., Goltry L., Tolentino E. K.R., Kas A., Larbig K., Lim Brody L.L., Coulter S.M., Folger K.R., Kas A., Larbig K., Lim Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T., Smith K.A., Spencer D.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                        01-MAR-2001
01-MAR-2001
01-DEC-2001
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-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTA.
                                                                                                                                                                                                                                                                                                                                                                                                               01-MAR-2001 (TrEMBLrel. 16, Created)
01-MAR-2001 (TrEMBLrel. 16, Last sequence update)
01-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PROBABLE SHORT-CHAIN DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                        Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Q913P2
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PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
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01-DEC-2001
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                                                                                                                                                                                                                                                                                            NCBI_TaxID=287;
                                                                                                                                                                                                                                                                                                                        Pseudomonas
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3L; AJ007731; CAA
3P; Q12634; 1YBV.
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(TremBLrel. 08, Last sequence up)
(TremBLrel. 19, Last annotation
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                  Q984V1;
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Q1-OCT-2001
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Q9KA03;
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STRAIN-C-125 / JCM 9153;
MEDIZINE-20512582; PubMed-11058132;
Takami H., Nakasone K., Takaki Y., Maeno G., Struji F., Hirama C., Nakamura Y., Ogasawara N.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Bacteria; Firmicutes; Bacillus/Staphylococcus
NCBI_TaxID-86665;
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Complete proteome; Oxidoreductase.
SEQUENCE 245 AA; 25365 MW; 342AlCF12C500744 CRC64;
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EMBL; AE004576; AAG04859.1;
HSSP; Q12634; 1YBV.
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Nature 406:959-964(2000).
-!- SIMILARITY: BELONGS T
                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome; Oxidoreductase.
SEQUENCE 246 AA; 26126 MW; 852B95EB8DEE9E90 CRC64;
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HSSP; P19992;
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Pfam; PF00106; adh_short; 1.
    PROBABLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRINTS; PROCOGO; SDRFAMILY.
PROSITE; PSCOCO61; ADH_SHORT; UNKNOWN_1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    halodurans and genomic sequence comparison Nucleic Acids Res. 28:4317-4331(2000).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Complete genome sequence of the alkaliphilic bacterium valodurans and genomic sequence comparison with Bacillu
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l Similarity 100.0%;
l0; Conservative (
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2001 (TrEMBLrel. 1
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E OXIDOREDUCTASE.
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red. No. 0.12;
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OS Rhizobium loti (Mesorhizobium loti).
OC Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
OC Phyllobacteriaceae; Mesorhizobium.

RN [1]
RN [2]
RN SEQUENCE FROM N.A.
RC STRAIN-MAFF303099;
RX MEDLINE-21082930; PubMed-11214968;
RX MEDLINE-21082930; PubMed-11214968;
RX MEDLINE-21082930; PubMed-11214968;
RX MERC T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
RA Kaneko T., Nakamura Y., Sato S., Asanizu E., Kato T., Sasamoto S.,
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RA Kaneko T., Nakamura Y., Sato S., Nakasahima K., Kimura T.,
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RA Kaneko T., Nakamura Y., Sato S., Nakasahima K., Kimura T.,
RA Kaneko T., Nakamura Y., Sato S., Nakamura Y., Sato
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OM protein - protein search, using sw model

Run on: tein search, using sw mouer.

Title: Perfect score: Sequence: 1 MAAPMNGQVCVVTGASRGIG.....YLPSFLRVPKWIIALYTSKF 313 US-10-006-163-1 313

Scoring table: OLIGO Gapop 60.0 , Gapext 60.0

105224 seqs, 38719550 residues

Word size : Searched: 0

Total number of hits satisfying chosen parameters:

105224

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

SwissProt\_40:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result<br>No. | Score | Query<br>Match L | Length I | DB       | ID           | Description                    |
|---------------|-------|------------------|----------|----------|--------------|--------------------------------|
| <b></b>       | 11.   | 3.5              | 271      | H        | NOR1_ASPPA   | Q00278 aspergillus             |
| ķ             | 10    | 3.2              | 244      | ь,       | FABG_ECOLI   | escherichi                     |
| ω             | 10    | •                | 244      | -        | FABG_SALTY   | salmon                         |
| 4             | 10    | •                | 244      | ۲        | FABG_VIBHA   | ibrio h                        |
|               | 10    | ٠                | 246      | μ.       | FABG_BACSU   | bacillu                        |
| σ             | 10    | •                | 249      | -        | DHK2_STRVN   | streptomyc                     |
| 7             | 10    | •                | 271      | ۳        | SDR1_PICAB   | picea abie                     |
| <b>6</b> 0    | 9     | ٠                | 244      | ٢        | FABG_VIBCH   |                                |
| ۰             | 9     | ٠                | 247      | μ        | FABG_PSEAE   | <ul> <li>pseudomona</li> </ul> |
| 10            | 9     | ٠                | 247      | 1        | FAG1_SYNY3   | P73574 synechocyst             |
| 1             | 9     | •                | 256      | -        | GNO_GLUOX    | gluconc                        |
| 12            | o ve  | ٠                | 320      | نہ،      | FABG_CUPLA   | cuphea lan                     |
| 1 5           | 0 0   | •                | 202      | 4 ـ      | I LVO_IEAST  | P4USBU Saccharomyc             |
| 15            | œ (   | 2.6              | 278      | - 1      | FIXR_BRAJA   | P05406 bradyrhizob             |
| 16            | 80    | •                | 319      | <b>—</b> | FABG_ARATH   | P33207 arabidopsis             |
| 17            |       | •                | 345      | _        | DCUP_RICPR   | rickettsi                      |
| 18            | . 60  | ٠                | 482      | -        | CLS2_BACSU   | P71040 bacillus su             |
| 19            | 000   | ٠                | 579      | -        | 2            |                                |
| 20            | 7     | ٠                | 106      | _ر       | YDFG_BACNO   | P39884 bacteroides             |
| 21            | 7     | •                | 138      | -        | HEX9_ADE07   |                                |
| 22            | 7     | ٠                | 145      | -        | ZUR_BACSU    | baci                           |
| 23            | 7     | ٠                | 173      | -        | HR12_MOUSE   |                                |
| 24            | 7     |                  | 185      | ۳,       | SV6          |                                |
| 2 2           | ,     |                  | 241      | -        | PHBB_ZOORA   | æ                              |
| 2 6           | ı ~   |                  | 240      | - ب      | FABG_THEMA   | 8 thermotoga                   |
| ) N           | ٦ -   |                  | 2 4      | - بـ     | HAH          | 0203 acinetobac                |
| , 6           | , ~   |                  | 240      | ٠,       | 1457   スコトリツ | 5                              |
| 2 0           | ı ~   | ٠                | 248      | ٠,       | DFG          | salmonella                     |
| 30            | 7     | ٠                | 251      | ш        | Y484_MYCTU   |                                |
| 31            | 7     |                  | 253      | بر       |              |                                |
| 32            | 7     |                  | 254      | -        | S            |                                |
| <u>u</u>      | 7     | 2.2              | 256      | -        | Y019_THEMA   | Q56318 thermotoga              |
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RESULT 2 FABG\_ECOLI

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| 485        | 459       | 427        | 383        | 316        | 314          | 294         | 292        | 289        | 287        | 261         | 261        |
| ۲.         | μ         | <u>ب</u>   | ۳          | Н          | μ.           | _           | ب          | <u> —</u>  | <b>-</b>   |             | <b>-</b>   |
| VST2_HEVRH | RCA_LYCPN | PYRC_BACCL | CYSL_SPIOL | TALA_ECOLI | LPPW_MYCTU . | E434_ADE02  | E434_ADE09 | PTR1_LEITA | PTR1_LEIMA | DHKR_STRCM  | ACT3_STRCO |
| 200270     | 049074    | P46538     | P32260     | P78258     |              | P03239      | P89083     | P42556     | Q01782     | P41177      | P16544     |
| hepatitis  | lycopersi | bacillus   | spinacia o | escherichi | mycobacte    | human adeno | human adei | leishmania | leishmania | streptomyce | streptomyc |

# ALIGNMENTS

| p Q                | 3 W O   |  | • |
|--------------------|---|--|---|
| VTGASRGIGRG 22<br> | 0.5%; Score 11; DB 1; Length 271; Best Local Similarity 100.0%; Pred. No. 0.0014; Matches 11; Conservative 0; Mismatches 0; Indels 0; Gaps 0; | NORL_ASPPA  NORL_ASPPA  NORL_ASPPA  NORL_ASPPA  NORL_ASPPA  NORL_ASPPA  NORL_ASPPA  NORL_OUTER  OUT  10-NOV-1997 (Rel. 35, Created)  DT  10-NOV-1997 (Rel. 35, Created)  DT  10-NOV-1997 (Rel. 35, Last sequence update)  DT  10-NOV-1997 (Rel. 35, Last sequence update)  DT  10-NOV-1997 (Rel. 35, Last sequence update)  DE  Aflatoxin blosynthesis ketoreductase NOR-1 (EC 1.1.1-).  NOR-1 OR NAR-1.  ANDR-1 OR NAR-1  ANDR-1 OR NAR-1.  ANDR-1 OR NAR-1  ANDR |   |

Query Match Best Local Matches

10; Similarity

3.2%; llarity 100.0%; Conservative

0, Score :

Mismatches . 10;

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Gaps

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DB 1; 0.014;

Length 244;

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CONFLICT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Yano M., HOZIUCHI.;
Yano M., HOZIUCHI.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 12,7-28.0 min region on the linkage map.";
DNA Res. 3:137-155(1996).
-1- CANTALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]
HADP(+) - 3-oxoacyl-[acyl-carrier protein] + NADPH.
-1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
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P25716; P78221;
O1-MAY-1992 (Rel. 2
O1-NOV-1997 (Rel. 3
16-OCT-2001 (Rel. 4
                                                                                                                                                                                                                                                                         EMBL; M84991; AAA23739.1; -.
EMBL; AE000210; AAC74177.1; -.
EMBL; D90745; BAA35901.1; -.
EMBL; B42147; B42147.
                                                                                                                                                                         EcoGene; EG11318; fabG.
InterPro; IPR002198; ADH_short.
Pfam; PF00106; Adh_short; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produbetween the Swiss Institute of Bioinformatics the European Bioinformatics Institute. There \varepsilon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A., Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K., Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K., Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Saito N. Sampei G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y., Yano M., Horiuchi T.;
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01-NOV-1997 (Rel. 35, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (EC 1.1.1.100) (3-ketoacyl-fabg OR B1093.
                                                                                                                                                                                                                                                                                                                                                                                                            or send
                                                                                                              Fatty
                                                                                                                                                                  PRINTS;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F., Gregor J., Dayls N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDIINE-92210530; PubMed-1556094;
Rawlings M., Cronan J.E. Jr.;
"The gene encoding Escherichia coli acyl carrier a cluster of fatty acid biosynthetic genes.";
J. Biol. Chem. 267:5751-5754(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-97061202;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STRAIN-K
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The complete genome sequence of Escherichia coll K-12."; science 277:1453-1474(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE-97426617;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (SDR) FAMILY.
                                                                                                                                   PR00080; SDRFAMILY.; PS00061; ADH_SHORT
                                                                                                                                                                                                                                                                                                                                                                                                    an email to license@isb-sib.ch).
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i blosynthesis; Oxidoreductase; NADP; Complet

10 34 NADP (BY SIMILARITY).

151 151 BY SIMILARITY:

30 30 A -> G (IN REF. 1).

244 AA; 25560 MW; 48EC1F2A7F7EEFD9 CRC64;
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                                                                                                                                ADH_SHORT; 1.
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SPECIES-S. typhi; STRAIN-CT18;

MEDLINE-21534947; PubMed-11677608;

MARCHINE-21534947; PubMed-11677608;

Parkhill J., Dougan G., James K.D., Thomson N.R., Pickard D., Wain J.

Churcher C., Mungall K.L., Bentley S.D., Holden M.T.G., Sebahhia M.,

Baker S., Basham D., Brooks K., Chillingworth T., Connerton P.,

Cronin A., Davis P., Davies R.M., Dowd L., White N., Farrar J.,

Feltwell T., Hamlin N., Haque A., Hlen T.T., Holroyd S., Jagels K.,

Krogh A., Larsen T.S., Leather S., Moule S., O'Gaora P., Parry C.,

Quall M., Rutherford K., Simmonds M., Skelton J., Stevens K.,

Whitchead S., Barrell B.G.;

Whitchead S., Barrell B.G.;
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30-MAY-2000
30-MAY-2000
                                                                                                                                                                                        -!- SIMILARITY: BELONGS
                                                                                                                                                                                                                                  -i- CATALITIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
-i- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                     "Complete genome sequence of a multiple enterica serovar Typhi CT18."; Nature 413:848-852(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 McClelland M., Sanderson K.E., Spieth J., Clifton S.W., La Courtney L., Porwollik S., Ali J., Dante M., Du F., Hou S. Leonard S., Nguyen C., Scott K., Holmes A., Grewal N., Mul Ryan E., Sun H., Florea L., Miller W., Stoneking T., Nhan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SPECIES-S. typhimurium: STRAIN-LT2;
MEDLINE-98317265; pubMed-9642179;
Zhang Y., Cronan J.E. Jr.;
"Transcriptional analysis of essential genes of the Escherichia fatty acid biosynthesis gene cluster by functional replacement w the analogous Salmonella typhimurium gene cluster.";
Ch. Bacteriol. 180:3295-3303(1998).
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30-MAY-2000 (Rel. 39, Last sequence update)
01-MAR-2002 (Rel. 41, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Waterston R., Wilson R.K.;
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FABG OR STM1195 OR STY1234.
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S., Layman D.,
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ACT_SITE
                                                                                                                                                                                                                                                                                                                                                                                                       Shen Z., Byers D.M.;

*Isolation of Vibrio harveyi acyl carrier protein; ";
and fabf genes involved in fatty acid biosynthesis; ";
J. Bacteriol. 178:571-573(1996).
-I- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]
NADP(+) = 3-oxoacyl-[acyl-carrier protein] +.NADPH.
-I- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
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                 Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAWILY.
PROSITE; PS00061; ADH_SHORT;
Fatty acid biosynthesis; Oxio
NP_BIND 10
34
                                                                                                                                         EMBL; U39441; AAC43589.1; -. HSSP; P19992; 1HDC.
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Bacteria; Proteobacteria;
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PROSITE; PS00061; ADH_SHORT; 1.
Fatty acid biosynthesis; Oxidoreductase; NADP;
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01-0CT-1996 (Rel. 34, Created)
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                                                                       use by non-profit institutions as long modified and this statement is not removed entitles requires a license agreement (See or send an email to license@isb-sib.ch).
                                                                                                                 This SWISS-PROT entry is copyright. It between the Swiss Institute of Bioinformatics Institute.
                                                                                                                                                                                           Oguro A., Kakeshita H., Takamatsu H., Nakamura K., Yaman
Submitted (MAR-1996) to the EMBL/GenBank/DBJ databases
- (- CATALYTIC ACTIVITY: (3R)-3-Nydroxyacyl-[acyl-carrier
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
- (- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOS
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"Bacillus subtilis acyl carrier pr
ilpid biosynthesis genes.";
J. Bacteriol. 178:4794-4800(1996).
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SEQUENCE 249 AA; 25977 MW; 922832B88FE34A8B CRC64;
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EMBL; X16144; CAA34262.1;
PIR; S05398; S05398.
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P16543;
01-AUG-1990
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PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
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01-AUG-1990 (Rel. 15, Last sequence update)
01-OCT-1996 (Rel. 34, Last annotation update)
Granaticin polyketide synthase putative keto
(EC 1.3.1.-) (ORF6).
Ractoria. Sirefundation value.
Ractoria. Sirefundation value.
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Sherman D.H., Malpartida F., Bibb M.J., Kieser H.M., Bibb
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Streptomycineae; Streptomycetaceae; St
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STRVN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Structure and deduced function of the granaticin-producing olyketide synthase gene cluster of Streptomyces violaceorul
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Hopwood D.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID-1935;
84 GRLDVLVNNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE
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PROSITE; PS00061; ADH_SHORT; FALSE_NEG.
                                                                      Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Pfam; PF00106;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12 VTGASRGIGR 21
|||||||||
9 VTGASRGIGR 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   O J. 8:2717-2725(1989).
PATHWAY: BIOSYNTHESIS OF THE POLYKETIDE ANTIBIOTIC GRANATICIN.
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                       l Similarity 100
10; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     acid
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9 33 NADP (BY SIMILARITY).
154 154 BY SIMILARITY.
23 D -> A (IN REF. 1).
246 AA; 26282 MW; C6A391167D3237DC CRC64;
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9
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                                  Score 10; DB; Pred. No. 0.0
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Pred. No.
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putative ketoacyl reductase
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                                                        DB 1;
0.014;
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0.014;
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                                                                           Length 249;
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SET TO SEE TO SE
        RESULT 8
FABG_VIBCH
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Best Local
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16-OCT-2001 (Rel. 40, Created)
16-OCT-2001 (Rel. 40, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (E
SEQUENCE FROM N.A.
STRAIN-EL TOR N16961 /
                                                                              Vibrio cholerae.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                                                   FABG_VIBCH
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ACT_SITE
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NP_BIND 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a c between the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and fo entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                               NCBI_TaxID=666
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002198; ADH_short. Pfam; PF00106; adh_short; 1. PRINTS; PR00080; SDRFAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; X74115; CAA52213.1; -. HSSP; Q12634; 1YBV.
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Ernst D.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
MEDLINE-94120027; PubMed-8290650;
Galliano H., Pfeiffer F.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  _PICAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Picea. NCBI_TaxID_3329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Plant Physiol. 103:1479-1480(1993)
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Picea abies (Norway spruce)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        "Isolation and characterization of short-chain alcohol dehydrogenase !
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Q08632;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                   Similarity 100.
10; Conservative
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271 AA;
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179
· 28724 MW;
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  SEROTYPE
                                                                              gamma subdivision;
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BY SIMILARITY.
, 743EAICBB2F85FE3 CRC64;
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om Norway spruce
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                                                                          Vibrionaceae;
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SEQUENCE FROM N.A.

STRAIN-AFCC 15692 / PAO1;

X MEDLINE-99395062; Pubmed-10464226;

X MEDLINE-9395062; Pubmed-10464226;

X KUtChma A.J., Hoang T.T., Schwelzer H.P.;

RT "Characterization of a Pseudomonas aeruginosa fatty aci
gene cluster: purification of acyl carrier protein (AC/
coenzyme A:ACP transacylase (fabb).";

coenzyme A:ACP transacylase (fabb).";
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FABG_PSEAE
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Best Local S
Matches 9
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Pfam; PF001(
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NP_BIND
ACT_SITE
                                                                                                                                                                                                                                                                                       FABG_PSEAE STANDARD; PRT; 247 AA 054438; 15-DEC-1998 (Rel. 37, Created) 15-DEC-1998 (Rel. 37, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat 3-oxoacyl-[acyl-carrier protein] reductase
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SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Dodson R.J., Haft D.H., Hickey E.K., Peterson J.D., Umayam L.A., Gll R., Nelson K.E., Read T.D., Tettelln H., Richardson D., Ermolaeva M.D., Vamathevan J., Bass S., Qln H., Dragol I., Sellers P. McDonald L., Utterback T., Fleischmann R.D., Nierman W.C., White O., Salzberg S.L., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C., Prince J.C., Smith H.O., Colwell R.R., Mekalanos J.J., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; AE004276; AAF95169.1; ALT_INIT.
TIGR; VC2021; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nature 406:477-483(2000).

1 - CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]

NADP(+) = 3-cxoacyl-[acyl-carrier protein] + NADPH.

1 - PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
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Heidelberg J.F., I
                                                                                                                                                                                                                               Bacteria; Proteobacteria;
                                                                                                                                                                                                                                               Pseudomonas aeruginosa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "DNA sequence of both chromosomes of the cholera pathogen
                                                                                                                                                                                                                                                                                                                                                                                                                                                  10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                12 VTGASRGIG
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PF00678; adh_short_C2; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Acid biosynthesis; Oxidoreductase; NADP; Complete

ND 10 34 NADP (BY SIMILARITY).

ITE 151 151 BY SIMILARITY.

NCE 244 AA; 25566 MW; 9FB2E8278D7CC3CE CRC64;
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9; Conser
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PubMed=10952301;
Eisen J.A., Nelso
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2.9%;
                                                                                                                                                                                                                                                                           reductase).
                                                                                                                                                                                                                                                                                        ast annotation update) protein] reductase (EC
                                                                                                                                                                                                                               gamma subdivision; Pseudomonadaceae;
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Pred. No.
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                                                                                        osa fatty acid
protein (ACP)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 244;
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SOLUTION DE LA PRESENTATION DE L
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FAGI_SYNY3 STANDARD; PRT; 247 AA.
ID FAGI_SYNY3 STANDARD; PRT; 247 AA.
AC P73574;
DT 15-DEC-1998 (Rel. 37, Created)
DT 15-DEC-1998 (Rel. 37, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE 3-cxoacyl-(acyl-carrier protein) reductase 1
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Best Local S
Matches 9
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MEDLINB-20437337; pubmed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.

Brody L.L., Coulter S.N., Folger K.R., Kest A., Larbig K., Lim R.M.

Smith K.A., Spencer D.H., Wong G.K.-S., Wu Z., Paulsen I.T.,

Reizer J., Saier M.H., Hancock R.E.W., Lory S., Olson M.V.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fatty aci
NP_BIND
ACT_SITE
SEQUENCE
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Nature 406:959-964(2000).
-i- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier pro-
NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.
-i- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTH
                                                                                                                                                                                                                    Hosouchi
Shimpo S.
Synechocystis sp. strain PCC entire genome and assignment DNA Res. 3:109-136(1996).
                                                                                                                                                                           Shimpo S., Tabata S.;
                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE-97061201; PubMed-8905231;
Kaneko T., Sato S., Kotani H., Ta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Synechocystis sp. (strain PCC 6803).
Bacteria; Cyanobacteria; Chroococcales;
NCBL_TaxID-1148;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL; U91631; AAB94395.1; -. EMBL; AE004722; AAG06355.1; -. HSSP; O12634; IYBV.
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FABG1 OR SLR0886.
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                                                                                                                                 "Sequence analysis
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SIMILARITY: BELONGS
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pr00080; SDRFAMILY.
pr00080; SDRFAMILY.
pr00061; ADH_SHORT; 1.
pr00061; ADH_SHORT; 1.
pr00061; ADH_SHORT; 1.
pr00080; SDRFAMILY.
pr00080; SDRFAMILY.
pr00080; SDRFAMILY.
pr00106; adh_short; 1.
pr00106; adh_s
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9; Conser
                                                                                                                                                                                                       N., Hirosawa M., Suglura M., Sasamoto S., Kin
T., Matsuno A., Muraki A., Nakazaki N., Naruc
, Takeuchi C., Wada T., Watanaha
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247 AA;
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                                                                                   of the genome of strain PCC6803. II
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25585 MW;
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AB83A2B95027445B CRC64;
                                     3. II. Sequence determination potential protein-coding regions
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                                         the unicellular cyanobacterium I. Sequence determination of the ential protein-coding regions.";
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                                                                                                                                                                                                                    Naruo K.
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                                                                                                                                                                                                                    , Kimura T.,
Naruo K., Okumu
ada M., Yasuda
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RESULT 11
GNO_GLUOX
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This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Exthe European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Klasen R., Bringer-Meyer S., Sahm H.;
"Blochemical characterization and sequence analysis of the gluconate:NADP 5-oxidoreductase gene from Gluconobacter ox. J. Bacteriol. 177:2637-2643[995].
-i-FUNCTION: INVOLVED IN THE NONPHOSPHORYLATIVE, KETOGENION OF THE NORTH O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GNO_GLUOX
P50199;
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ACT_SITE
SEQUENCE
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STRAIN-DSM 3503;
MEDLINE-95270576; PubMed-7751271;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-OCT-1996 (Rel. 34, Creat
01-OCT-1996 (Rel. 34, Last
16-OCT-2001 (Rel. 40, Last
Gluconate 5-dehydrogenase (
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NP_BIND 11 35 NADP (BY SIMILARITY).
ACT_SITE 156 156 BY SIMILARITY.
SEQUENCE 247 AA; 25724 MW; 91EBF9409C777F20 CRC64;
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PROSITE; PS00061; ADH_SHORT; 1.
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Pfam; PF00106; adh_short; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            luconobacter oxydans (Gluconobacter suboxydans).
actaria; Proteobacteria; alpha subdivision; Acetobacteraceae;
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                                                                                                                                                                                                                                                                                                                                          OF GLUCOSE AND OXIDIZES GLUCONATE TO 5-KETOG NADD, ALMOST INACTIVE WITH NAD. CATALYTIC ACTIVITY: D-gluconate + NAD(P)(+) gluconate + NAD(P)H. SUBUNIT: HOMODIMER.
                                                                                                                                                                                                                                                                             SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE OF 3-19,
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Last annotation update)
Lase (EC 1.1.1.69) (5-keto-D-gluconate
                                                                                                                                                                                                                                          4: Cytoplasmic.
TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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                                  There are no restrictions ong as its content is in
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Best Local
                                                                                                                                                                                         use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entitles requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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01-DEC-1992 (Rel. 24, Created)
01-DEC-1992 (Rel. 24, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-2001 (Rel. 40, Last annotation update)
Carrier protein] reductase, chloroplast precursor
                                                                                                       EMBL; X64566; CAA45866.1;
PIR; S19832; S19832.
HSSP; P50162; 1AE1.
                                                                                                                                                                                                                                                                              This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute. There are no restricted to the swing of the content of the swing o
                                                                                                                                                                                                                                                                                                                                                                                                                                                PATHWAY.
-!- SUBUNIT: HOMOTETRAMER (PROBABLE).
-!- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MOI. Gen. Genet. 233:122-128(1992).

-I- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]

NADP(+) - 3-oxoacyl-[acyl-carrier protein] + NADPH.

-I- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eucosids II; Myrtales; Lythraceae; Cuphea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta-ketoacyl-ACP reductase.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CUPLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Klein B., Pawlowski K.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-92293104;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cuphea lanceolata.
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ACT_SITE
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Oxidoreductase; NADP.
39
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9; Conserv
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27256 MW;
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0; Mismatches
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BY SIMILARITY.
; 38B03C0399C0A07A CRC64;
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PRINTS; PR00080; SDRFAMILY. PROSITE; PS00061; ADH\_SHORT

biosynthesis;

Oxidoreductase;

NADP; Chloroplast;

InterPro; IPR002198 Pfam; PF00106; adh\_

IPR002198; ADH\_short.

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RESULT
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P40580;
01-FEB-1995
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                 Hypothetical | NP_BIND ACT_SITE 1: SEQUENCE 26:
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Barrell B.G., Badcock K., Bankier A.T., Bowman S., Brown D.,
Churcher C.M., Connor R., Copsey T., Dear S., Deviln K., Fraser
Gentles S., Hamlyn N., Horsnell T.S., Hunt S., Jagels K., Jones
Louis E., Lye G., Moule S., Moule T., Odell C., Pearson D.,
Rajandream M.A., Riles L., Rowley N., Skelton J., Smith V.,
Walsh S., Whitehead S.;
Submitted (DEC-1994) to the EMBL/GenBank/DDBJ databases.

Submilarity: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   U1-FEB-1995 (Rel. 31, Last s
16-OCT-2001 (Rel. 40, Last a
Hypothetical oxidoreductase
(EC 1.-.-).
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TRANSIT
                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a cobetween the Swiss Institute of Bioinformatics and the EMBL the European Bioinformatics Institute. There are no restrict use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and for entitles requires a license agreement (See http://www.isb-sib.or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Eukaryota; Fungi; / Saccharomycetales;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae
                                                                                                                                                                                                                                                            InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A
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82 VTGASRGIG
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nes 9; Conserv
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                                                                                                                                                                                                                                                                                                                            ; Z38061; CAA86196.1; -. S48498; S48498.
S00001475; XIRO36C.
                                      TGASRGIG
TGASRGIG
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                                                                             8; Conserv
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263 A
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227
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larity 100.0%;
Conservative
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157
28804
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Ascomycota; Saccharomycotina; Saccharomycetes;
; Saccharomycetaceae; Saccharomyces.
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O NAD OR NADP (BY SIMILARITY).

O BY SIMILARITY.

18804 MW; 53DE25425AAC946F CRC64;
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MBL outstation -
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RESULT 14
DHCA_HUMAN
ID DHCA_HUMAN
AC P16152;
Gabbay K.H.;
"Human carbonyl reductase. Nucleotide sequence amino acid sequence of the encoded protein.";
J. Biol. Chem. 263:16185-16188(1988).
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Carbonyl reductase [NADPH] 1 (EC 1.1.1.184) (EC 1.1.1.189)
reductase 1) (Prostaglandin-E2 9-reductase) (EC 1.1.1.189)
(Prostaglandin 9-ketoreductase) (15-hydroxyprostaglandin dehydrogeting (NADP+)) (EC 1.1.1.197).
CBR1 OR CBR OR CRN.
Homo sapiens (Human).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Ramser J., Beck A., Klages S., Hennig S., Riesselmann L., Wehrmeyer S., Borzym K., Gardiner K., Nizetic D., Francis Lehrach H., Reinhardt R., Yaspo M.-L.;
"The DNA sequence of human chromosome 21.";
Nature 405:311-319/2000
                                                                        Hattori M., Fujiyama A., Taylor T.D., Watanabe H., Yada T., Park H.-S., Toyoda A., Ishii K., Totloki Y., Choi D.-K., Soeda E Ohki M., Takagi T., Sakaki Y., Taudien S., Blechschmidt K., Pol Menzel U., Delabar J., Kumpf K., Lehmann R., Patterson D., Reichwald K., Rump A., Schillhabel M., Schudy A., Zimmermann W. Rosenthal A., Kudoh J., Shibuya K., Kawasaki K., Asakawa S., Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis Shintani A., Sasaki T., Nagamine K., Mitsuyama S., Antonarakis Minoshima S., Shimizu N., Nordsiek G., Hornischer K., Brandt P. Scharfe M., Schoen O., Desario A., Reichelt J., Kauer G., Bloec Bassari T., Shoen O., Desario A., Reichelt J., Kauer G., Darah
                                                                                                                                                                                                                                                                                                                                                                             Watanabe K., Sugawara C., Ono A., Fukuzumi Y., Itakura Yamazaki M., Tashiro H., Oscegawa K., Soeda E., Nomura "Mapping of a novel human carbonyl reductase, CBR3, and pseudogenes to human chromosome 21q22.2."; genomics 52:95-100(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Forrest G.L., Akman S., Doroshow J., Rivera H., Kaplan W.D.; "Genomic sequence and expression of a cloned human carbonyl gene with daunorubicin reductase activity."; Mol. Pharmacol. 40:502-507(1991).
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01-APR-1993 (Rel.
16-OCT-2001 (Rel.
                                                                                                                                                                                                                                SEQUENCE FROM N.A. MEDLINE-20289799; PubMed-10830953;
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Doroshow J., Felsted R.L., Mohandas T., Bachur N.R.;
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RESULT 15
FIXR_BRAPA
ID FIXR_B
AC P05406
DT 01-OCT
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DE F1xR P
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Bradyrhizobium japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizobium group; Bradyrhizobium.
                                                                            FIXR_BRAJA STANDARD; PRT; 278 AA. P05406; 01-NOV-1988 (Rel. 09, Created) 01-OCT-1989 (Rel. 12, Last sequence update) 01-OCT-1996 (Rel. 34, Last annotation update)
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Carboxyethyllysine in a protein: native carbonyl reductase/NADP(+)-

dependent prostaglandin dehydrogenase.";

Proc. Natl. Acad. Sci. U.S.A. 90:502-506(1993).

-I- FUNCTION: CATALYZE THE REDUCTION OF A WIDE VARIETY OF CARBONYL

COMPOUNDS INCLUDING THE ANTITUMOR ANTHRACYCLINE ANTIBIOTICS.

CAN CONVERT PROSTAGLANDIN EZ TO PROSTAGLANDIN EZ-ALPHA.

-I- CATALYTIC ACTIVITY: R-CHOH-R' + NADP(+) = R-CO-R' + NADPH.

-I- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-9,11,15-trihydroxy-9-oxoprosta-

-i- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-11,15-dihydroxy-9-oxoprosta-

-i- CATALYTIC ACTIVITY: (5Z,13E)-(15S)-11,15-dihydroxy-9-oxoprosta-
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PROSITE; PS00061; ADH_SI
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MEDLINE-93133816;
Krook M., Ghosh D
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CATALYTIC ACTIVITY: (5Z,13E)-(15S)-11-alpha,15-dihydroxy-9-oxoprost-13-enoate + NADPH.
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SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
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276 AA;
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Matches 8
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                                                                                                    Nitrogen fixation; Oxidoreductase.
NP_BIND 40 64 NAD CACT_SITE 189 189 BY SI
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Pfam; PF00106; adh_short; 1.
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8; Conser
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189
278 AA;
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29715 MW;
                                    2.6%;
                                   Score 8; 1; Pred. No.
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Result
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#### nitochondria; immune disorder; cancer; leukemia; adenocarcinoma; lymphoma; breast; lung; testis; prostate; brain; Addison's disease; acquired immune deficiency syndrome; asthma; anemia; Crohn's disease; Graves disease; AIDS; gene therapy. WPI; 1999-429503/36. N-PSDB; AAX86772. 05-FEB-1998; Short-chain dehydrogenase; HSCD; enzyme; AAY27004 standard; Protein; 313 05-FEB-1998; 27-JUL-1999. US5928923-A. Human short-chain dehydrogenase (HSCD) enzyme 20-SEP-1999 (first entry) AAY27004; Corley NC, Homo sapiens. (INCY-) INCYTE PHARM Lal P; 98US-0019216 98US-0019216 INC. pyruvate; coenzyme A; human;

Nucleic acids encoding human short chain dehydrogenase enzymes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      dehydrogenase enzymes catalyse an irreversible reaction between pyruvate and coenzyme A, to form CO2 and the intermediate COA, in mitochondria. Host cells containing vectors comprising the HSCD nucleic acid may be used to produce the HSCD enzyme, according to standard recombinant DNA methodology. The enzyme may then be used as an antigen in the production of antibodies or in assays to identify antagonists of HSCD activity. These antagonists may then be used to treat disorders associated with inappropriate expression, or over activity of HSCD such as immune disorders and coenzyme A). For example, the antagonists may be used to treat leukemia, lymphomas, adenocarcinomas and cancers of the breast, lung, testis, prostate and brain, Addison's disease, acquired in mene deficiency syndrome (AIDS), asthma, anemia, Crohn's disease and coraves disease. The nucleic acids and antisense sequences can be used to mene thereave.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
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Matches 313
                 Human; open reading frame; ORFX; detection; cytostatic; hepatotropic; vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antiviral; antienterial; antimunosuppressive; antiinflammatory; antiarterial; antienterial; antienterial; antienterial; antienterial; antienterial; antienterial; gene therapy; cancer; proliferative disorder; hyportension;
                                                                                                                                                                                          08-FEB-2001
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                                                                                                                                                    ORFX ORF2404 polypeptide sequence
                                                                                                                                                                                                                                                          standard; Protein;
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Pred. No. 5.le-164;
); Mismatches 0;
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proliferative disorder;
rthritis; graft vs host (
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nvglrghyfcsvygarlmvpagqgl1vv1sspgslqymfnvpygvgkaacdklaadcahe

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61 61 Query Match Best Local s Matches 312

Local Similarity hes 312; Conserv

Conservative

1;

Score 1619; DB 21; Pred. No. 1.3e-163; 1; Mismatches 0;

Indels Length

0;

Gaps

0

99.8%;

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CC AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB43397, CC which represent the human ORFX open reading frames 1 to 3161. The ORFX CC sequences have activities such as: cytostatic; hepatotropic; vulnerary; CC antipsoriatic; antiparkinsonian; nootropic; neuroprotective; costeopathic; anticonvulsant; thrombolytic; coagulant; vasotropic; immunostimulant; cardiant; thrombolytic; coagulant; vasotropic; cc antidiabetic; hypotensive; dermatologica; immunosuppressive; cc antityroid; and antianaemic. The sequences can be used for determining cc the presence of or predisposition to, or preventing or treating cc the presence of or predisposition to, or preventing or treating cc nucleic acids can be used to express ORFX proteins in gene therapy cectors. The proteins and nucleic acids may be used to treat cancers, cc proliferative disorders, neurodegenerative disorders, osteoarthritis, cc praft vs host disease, cardiovascular disease, diabetes mellitus, hypothyroidism, cholesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, cc allergies, aplastic anaemia, burns, wounds, bone and cartilage damage, cc coagulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                31-MAR-1999;
02-APR-1999;
05-APR-1999;
30-MAR-2000;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim
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DB; AAC76849.
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                                                                                                                                                                                                     This invention relates to purified human proteins AAB81047 - AAB81056 which are encoded by cDNA sequences AAF77476 : AAF77485. The invention includes an expression vector which can translate DNA encoding the protein or express it in a cell. Also included is a cell transformed by the vector, and an antibody specific for the protein. The protein can be used for the detection of receptors and ligands and in the screening for new low molecular weight drugs. The present sequence represents the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; HP00758; low molecular weight drug.
                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                          Novel protein useful for the detection of for screening low molecular weight drugs
                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                      2001-285599/30.
DB; AAF77480.
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vpkwiialytskf 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein HP01017 amino acid sequence
                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                     35pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            protein;
                                                                                                                                                                                             the human cDNA clone HP00758.
                                                                                                                                 99.8%;
99.7%;
                                                                                                                                                                                                                                                                                       Japanese
                                                                                                                                                                                                                                                                                                                                                                     SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            313 AA
                                                                                                                               Score 1619; DB 22; Pred. No. 1.3e-163;
                                                                                                                        Mismatches
                                                                                                                                          DB 22; Length
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                                                                                                                                                                                                                                                                                                                    receptor and
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                                                                                                                                                                                                               The protein can be the screening for
                                                                                                                                            313;
                                                                                                                                                                                                                                                                                                                    a ligand,
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                                                                      AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psordasis; sepsis; diabetes; atherosclerosis; skin disorder; angiogenic disorder; kidney disorder; cardiovascular disorder; angiogenic disorder; kidney disorder; angiogenic disorder; kidney disorder.
   proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune sys AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammatic
                                                                                                                                                                                                                                                                                                                                                                                                                   Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-NOV-1999;
27-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000; 2000WO-US30653.
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cell culture; chemotaxis; food additive
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           241
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                                                                                                                                                                                                                                                                                                                                                                                                                Page 549; 60%pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        22-encoded secreted protein HHFCZ67, SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Komatsoulis
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2000US-0221193.
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(e.g.,
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on; wound healing;
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disorder; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          vulnerary;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Moore
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ID NO:195
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                              system,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CC allergies, neurological disorders (e.g., Alzheimer's disease, Parkinsons's disease), cognitive disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC cardiovascular disorders, angiogenic disorders, kidney disorders, CC gastrointestinal disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound CC sunburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used CC as a food additive or preservative to modify storage properties. CC alleviating symptoms associated with the disorders mentioned above, and communosorbent assay (ELISA). The present sequence represents a human ver construction of the invention can be used to communosorbent assay (ELISA). The present sequence represents a human ver construction of the invention can be used to communosorbent assay (ELISA). The present sequence represents a human ver construction of the invention.
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Best Local Similarity
Matches 144; Conserv
                                                                                                                                                                                                                                                                             Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoietic disorder; inmune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; satiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary;
     Ruben SM,
                                                                                                                   08-NOV-2000; 2000WO-US30653
                                                                  12-NOV-1999; 99US-0164735,
27-JUL-2000; 2000US-0221193,
                                                                                                                                                         17-MAY-2001
                                                                                                                                                                                         WO200134628-A1
                                                                                                                                                                                                                                                                       endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                            Homo sapiens
                                                                                                                                                                                                                                                              binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human gene 22-encoded secreted protein fragment; SEQ ID NO:254.
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                                                                                                                                                                                                                                                          partner identification.
Komatsoulis GA,
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100.0%; Pred. No. 4.6e-71
tive 0; Mismatches 0
Birse CE,
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AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted CC protein genes, and AAG73346-AAG73448 represent the proteins they encode. CC AAG73449-AAG73519 represent human secreted proteins are useful for preventing, cc treating or ameliorating medical conditions, e.g., by protein or genee CC amount of the new protein in a sample or by determining the CC amount of the new genes. Specific uses are described for each of the CC and include developing products for the diagnosed by determining the CC and include developing products for the diagnosis or treatment of CC and include developing products for the diagnosis or treatment of CC abnormalities, haematopoietic disorders, diseases of the immune system, cancer, tumours, foetal and developmental CC abnormalities, haematopoietic disorders, diseases of the immune system, can also represent the companies of the immune system, can disorders (e.g., Alzheimer's disease, cancer, tumours, foetal and developmental cC allergies, neurological disorders (e.g., Alzheimer's disease, candiovascular disorders, pregnancy-related disorders, atherosclerosis, candiovascular disorders, pregnancy-related disorders, and infections. The proteins can also be used to aid wound the protein and infections. The proteins can also be used to aid wound constant proliferation, to prevent skin aging due to constant ligands or binding partners, and in chemotaxis, and can be used to aid antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radiommunoassay or enzyme linked cc inmunoassays e.g., radiommunoassay or enzyme linked cc immunoassays e.g., radiommunoassay or enzyme linked cc secreted protein fragment referred to in the discreers a human such and can be used in induspriate protein fragment referred to in the discreers a human such and can be used in induspriate protein assay (ELISA). The present sequence represents a human such assay (ELISA). The present sequence of the invention.
Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
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Best Local
                                                                10-AUG-2001
                                                                                    AAG73481;
                                                                                                    AAG73481 standard; Protein;
                                                                                                                                                   304 WITALYTSKF 313
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118 witalntskf 127
                                                                                                                                                                                             244 NILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSGLGWLASYLPSELRVPK 303
                                                                                                                                                                                                                                           193 PGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSS-AETTELSGKCV-----VALATDP 243
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                                                                                                                                                                                                                                                                      82;
                                         22-encoded secreted protein fragment,
                                                              (first entry)
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                                                                                                                                                                                                                                                                  Score 371; DB 22;
Pred. No. 2.8e-31;
6; Mismatches 12
                                                                                                                                                                                                                                                                                     Length
                                                                                                                                                                                                                                                                                     127;
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                                                                                                                                                                                                                                                                Gaps
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Moore

PA;

Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;

ase; rheumatoid arthritis;
Alzheimer's disease;

SEQ ID NO:256

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CC and their corresponding secreted proteins are useful for preventing.

CC treating or ameliorating medical conditions, e.g., by protein or gene

CC therapy. Pathological conditions can be diagnosed by determining the

CC amount of the new protein in a sample or by determining the presence of

CC mutations in the new genes. Specific uses are described for each of the

CC genes, based on the tissues in which they are most highly expressed,

CC and include developing products for the diagnosis or treatment of

CC proliferative disorders, cancer, tumours, foetal and developmental

CC and include developing products for the diagnosis or treatment of

CC proliferative disorders, cancer, tumours, foetal and developmental

CC allergies, neurological disorders (e.g., Place arthritis), inflammation,

CC allergies, neurological disorders (e.g., Alzheimer's disease,

CC parkinsons's disease), cognitive disorders, schizophrenia, asthma,

CC parkinsons's disease), cognitive disorders, schizophrenia, asthma,

CC gastrointestinal disorders, pregnancy-related disorders, endocrine

CC disorders, and infections. The proteins can also be used to aid wound

CC disorders, and infections. The proteins can also be used to aid wound

CC culture of primary tissues, to regenerate tissues, to identify their

CC cognate ligands or binding partners, and in chemotaxis, and can be used

CC alleviating symptoms associated with the disorders mentioned above, and

CC alleviating symptoms associated with the disorders mentioned above, and

CC alleviating symptoms associated with the disorders mentioned above, and

CC alleviating symptoms associated with the disorders mentioned above, and

CC alleviating protein fragment referred to in the disclosure of the invention.
                                                                                                                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Parkinson's disease; cognitive disorder; schizophrenia; skin disorder; psoriasis; sepsis; diabetes; atherosclero cardiovascular disorder; angiogenic disorder; kidney dis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-NOV-1999; 99US-0164735.
27-JUL-2000; 2000US-0221193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              08-NOV-2000; 2000WO-US30653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-MAY-2001
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                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein genes, and AAG73346-AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
                                                                                                                                                                                       Local
partner identification.
                                                                                                                                                                                       Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                               72
                                                                                                                                                            Conservative
                                                                                                                                                                                       22.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Birse CE,
                                                                                                                                                    Score 361; DB 22; I
Pred. No. 1.3e-30; .
0; Mismatches 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Νi J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Moore
                                                                                                                                                                                                                      Length 72;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ·.·
                                                                                                                                                        Indels
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302

PKWIIALYTSKF

Query Match
Best Local Similarity
Matches 120; Conserv

Conservative

35;

21.28;

Score 344; DB 22; Pred. No. 8.4e-28; 5; Mismatches 92;

Length 303; Indels 102;

Gaps

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Sequence

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AAB9502
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                                                                               CC to the 5602 nucleotide sequences defined in the specification, where the CC oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprises at least 15 nucleotides; or (b) a combination CC of an oligonucleotide comprising a sequence complementary to the CC complementary strand of a polynucleotide which comprises a 5'-end CC complementary to a combination CC complementary strand of a polynucleotide which comprises a 5'-end sequence complementary to a CC polynucleotide which comprises a 3'-end sequence complementary to a CC configuration of the 5'-end sequence/3'-end sequence is selected from those defined in CC the 5'-end sequence/3'-end sequence is selected from those defined in CC in gene therapy. The primers are useful for synthesising polynucleotides, CC particularly full-length cDNAs. The primers are also useful for the CC in gene therapy and comprise of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length CDNAs easily without any specialised methods. AAH33162 to AAH3363 to AAH318742 represent human cDNA sequences; AAB92446 to CC captesent oligonucleotides, all of which are used in the exemplification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ota T,
Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Primer sets for synthesizing polynucleotides, particularly the 5602 full-length cDNAs defined in the specification, and for the detection, and for the abnormality of the proteins encoded by the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAB95802 standard; Protein; 303 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer se
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Claim 8;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              and/or diagnosis of the full-length cDNAs -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       09-JUN-2000;
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02-MAY-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              29-JUL-1999;
27-AUG-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                07-FEB-2001.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human; primer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein sequence SEQ ID NO:18783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  26-JUN-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAB95802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprises: (a) an oligo-dT primer and an oligonucleotide complementary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HELI-) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               52
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|pkwiialntskf 72
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Sugiyama
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID 18783;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      99JP-0248036
                                                               invention
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T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2537pp + CD ROM;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hayashi K, S
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K, Otsuki
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for the detection encoded by the
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               Matches
                                        Query Match
Best Local :
                                                                                                                                                                      The invention relates to gene encoding D-arabinitol dehydrogenase, isolated from Bacillus sp. IKD-5A868 strain. The protein can be expressed by standard recombinant methodologies. D-arabinitol dehydrogenase is used as a clinical diagnosing agent for mycosis. The present sequence represents the D-arabinitol dehydrogenase enzyme.
                                                                                                                                       Sequence
                                                                                                                                                                                                                                                                                                                       Claim 1; Page 10-11; 14pp; Japanese.
                                                                                                                                                                                                                                                                                                                                                                Arabinitol dehydrogenase gene encoding D-arabinitol useful as a clinical diagnosing agent for mycosis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Bacillus D-arabinitol dehydrogenase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (NIPK ) NIPPON KAYAKU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      26-MAY-1998;
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               Local Similarity
les 72; Conserv
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DB; AAZ46762, AAZ46763
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            standard; Protein; 258
                                                                                                                                       258
          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     dehydrogenase; clinical diagnosis; mycosis
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33; Mismatches
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  l. 1e-20;
les 87;
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  Indels
                                                   Length
                                                                                                                                                                                                                                                                                                                                                                                       dehydrogenase
  15;
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5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64

immune system

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RESULTANGE AND ANAGORDANA ANAGORD
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                                                           AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the protein or sample or by determining the formutations in the new genes. Specific uses are described for each of the and include developing products for the diagnosis or treatment of and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                      Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI;
                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Page 47; 604pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            12-NOV-1999;
27-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        endocrine disorder; infection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gastrointestinal disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human gene 22-encoded secreted protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   483
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ELRRHGVSCVSLWPGIVQTELLKEHMA 206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     nsvflmskaagkvmirqgkgsiinissmsgl--ivntpqpqaaynvskagvimltkslas 178
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2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                               English.
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tumours, icc
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AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammati allergies, neurological disorders (e.g., Alzheimer's disease, Parkhisons's disease), cognitive disorders, schizophrenia, asthma, ethn.disorders (e.g., asthma, asth

inflammation,

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Query Match
Best Local Similarity
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73485
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                                                                                                                                                                                                                                                                                                                                                       Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoletic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; gastrointestinal disorder; pregnancy-related disorder; tumour;
                                                                                                                                                                                                                                                                                                                            endocrine disorder; infection;
cell culture; chemotaxis; food
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAG73485 standard; Protein; 68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
                                                                                                                 12-NOV-1999; 99US-0164735.
27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAG73485
                                                                                                                                   12-NOV-1999;
                                                                                                                                                                     08-NOV-2000; 2000WO-US30653.
                                                                                                                                                                                                         17-MAY-2001
                                                                                (HUMA-) HUMAN GENOME SCI INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                170 CDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQF-KSAFSSAET
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           72 rgv-glc1------lnnkiryshspgaycgrcraehgthiisfnpvre 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELSGKCVVALATDPNILSLSGKVLPS-----CDLAR-RYGLRDVDGRPVQD 274
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              62;
                                                                                                                                                                                                                                                                                                            partner
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                                                Komatsoulis GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                            identification
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Pred. No. 3
                                                                                                                                                                                                                                                                                                                                         wound healing; vulnerary;
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                                                CE,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NO:260
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Sequence

83

AA;

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Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy
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Disclosure; Page 47; 604pp; English.

CC AIDS, autolumne diseases (e.g., rheumatoid arthritis), inflammation, (C allergies, neurological disorders (e.g., Alzheimer's disease, eurological disorders (e.g., Alzheimer's disease, cognitive disorders, schizophrenia, asthma, cc skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, cc cardiovascular disorders, angiogenic disorders, kidney disorders, cc cardiovascular disorders, angiogenic disorders, kidney disorders, cc disorders, and infections. The proteins can also be used to aid wound chealing and epithelial cell proliferation, to prevent skin aging due to culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used cas a food additive or preservative to modify storage properties. CC antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and can decrease in the disorders mentioned above, and continuous corrected protein fragment referred to in the disorders mentioned above a munosorbent assay (ELISA). The present sequence represents a human cc secreted protein fragment referred to in the disclosure of the invention. AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346 AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the disposis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, proteins they encode.
fragments. The derry

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                                                                                                    Query Match
Best Local Similarity
                                                         170 CDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHWAKEEVLQDPVLKQF-KSAFSSAET 228
                       229 TELSGKCVV 237
   61
                                             μ
rgv-glcil 68
                                             cdklaadcahelrrhgvscvslwpgivqtellkehmakeevlqdpvlkqvgkgrakeaen
                                                                                           54;
                                                                                           Conservative
                                                                                                   16.4%;
78.3%;
                                                                                           ω
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                                                                                                   Score 266; DB 22;
Pred. No. 1.6e-20;
                                                                                           Mismatches
                                                                                                                Length
                                                                                          Indels
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                                                                                           Gaps
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RESULT
AAY54422
ID AAY
XX
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AAY54422 standard; Protein; 248

06-APR-2000 (first entry)

Amino acid sequence of a beta-ketoacyl-ACP reductase protein

steroselectivity; 4-chloroacetoacteic acid ester; (S)-4-halo-3-hydroxybutyric acid ester; beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-CoA reductas beta-ketoacyl-acyl carrier protein reductase; acetoacetyl-C
polybeta-hydroxy fatty acid biosynthesis; optically active; Beta-ketoacyl-ACP reductase; Type II fatty acid synthetase; 4-haol-3-hydroxybutyric

Bacillus subtilis

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RESULT 1
ABB59275
ID ABB5
XX ABB5
XC ABB5
XX
AC ABB5
XX
DT 26-P
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DE Dros
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DF Dros
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Best Local
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                                           Drosophila; developmental biology; cell signalling; insecticide;
                                                                                                                           Drosophila melanogaster polypeptide SEQ ID NO 4617
                                   pharmaceutical.
                                                                                                                                                                                                                          26-MAR-2002
                                                                                                                                                                                                                                                                                                         ABB59275;
                                                                                                                                                                                                                                                                                                                                                                 ABB59275 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             constituting Type II fatty acid synthase, or acetoacetyl-CoA reductase constituting the polybeta-hydroxy fatty acid biosynthesis system. The novel method is used to produce optically active 4-haol-3-hydroxybutyric acid ester, with a high purity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           08-MAY-1998;
21-OCT-1998;
05-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           acid ester. The specification describes a method for product (S)-4-halo-3-hydroxybutyric acid ester. The method comprises
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           a Type II fatty acid synthetase. The enzyme has an extremely high reducing activity and steroselectivity towards 4-chloroacetoactein acid error who provides the control of the control of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence represents a beta-ketoacyl-ACP reductase of Bacillus subtilis. The beta-ketoacyl-ACP reductase enzyme of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Producing optically pure (S)-4-halo-3-hydroxybutyric acid ester
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N-PSDB; AAZ45749.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         248 AA;
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98JP-0300178.
99JP-0098205.
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Pred. No. 3e-18;
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Best Local 9
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                                             AAW02111;
                                                             AAW02111 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The inventiuseful in developmental biology and in elucidating cell signalling cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL305737-ABB72072).
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The sequence data specification, but
                                                                                                                                                                                                                                                                                                                                                                                                                                                  at ftp.wipo.int/pub/published_pct_sequences.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 4617; 21pp + Sequence Listing; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated nucleic acid genes from Drosophila and interactions -
                                                                                                                                                 229 TELSGKCVVALATD 242
                                                                                                                          235 deasfstgislpvd 248
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11-JUL-2000;
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                                                                                                                                                                                                                                                                                                                                      8 QVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGG-QCVPVVCDSS
                                                                                                                                                                     pkgvrvnsvnpgviitelqrrggldqeayvkflehakvthalgrpgevkevaaaiaflas
                                                                                                                                                                                                RHGVSCVSLWPGIVQTELLK-----
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DB; ABL03378.
                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                              257 AA;
                                                                                                                                                                                                                                                                                                                                                                   Conservative
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2000US-0614150
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                                                                                                                                                                                                                                                                                                                                                                              14.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             detection reagent for detecting for elucidating cell signalling
                                                                                                                                                                                                                                                                                                                                                                   40;
                                                                 256 AA
                                                                                                                                                                                                                                                                                                                                                                 Score 227.5; DB 22;
Pred. No. 1.7e-15;
0; Mismatches 105;
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and cell-cell
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19

Gluconate: NADP+-5-oxidoreductase

06-MAR-1997

(first entry)

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RESULT 1
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              5-keto:gluconate prodn. by increasing expression of gluconate: NADP+-5-oxido:reductase gene - esp. by increasing copy no. in Gluconobacter, used as intermediate for ascorbic and tartaric acids
                                    Rape; leaf; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase; plasmid pJR16.2; cDNA library; Escherichia coli; vector; plastid; stroma; transit peptide; cassette; antisense; oliseed; transgenic plant; crop improvement; lipid; metabolic engineering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The gluconobacter oxydans gene may be used to transform cells, to produce higher levels of gluconate.

Tartaric acid can now be produced without the difficult purification involved in prepn. from tartar.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 8; Page 10-12; 15pp; German.
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N-PSDB; AAT36145.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gluconobacter oxydans
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gluconate; NADP; oxidoreductase; Gluconobacter oxydans; ascorbic acid; tartaric acid; ds.
                                                                                                                               13-APR-1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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Brassica napus
                         polymer; rapeseed
                                                                                                     Rape leaf beta-ketoacyl-ACP-ketoreductase.
                                                                                                                                                         AAR89323
                                                                                                                                                                                 AAR89323 standard; Protein;
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                                                                                                                                                                                                                                                                                                  navffvgqavarhmiprgrgkivnicsvqselarpgi-----apytatkgavknltkgm 174
                                                                                                                                                                                                                                                                                                                              RGHYFCSVYGARLMVPAGQGLIVVISS-----PGSLQYMFNVPYGVGKAACDKLAADC
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                                                                                                                                                                                                                                                                                                                                                                                  SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL 124
                                                                                                                                                                                                                                                                                                                                                                                                            lsgaralvtgasrgigltlakglarygaevvlngrnaesldsagsgfeaeglkastavfd 68
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Pred. No. 5.6e-15;
""" tches 93;
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                                    metabolic engineering;
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RESULT 1

AAR89322

standard;

Protein;

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AAR89322; 13-APR-1996

(first entry)

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                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local Similarity
Matches 75; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The sequence corresponds to a rape leaf beta-ketoreductase encoded by a cDNA insert in plasmid pJRL6.2 in Escherichia coli XII-Blue. A plastid stroma targeting transit peptide is present. DNA encoding the protein may be inserted in a vector or expression cassette in sense or antisense orientation for expression in an oilseed plant, e.g. for production of transgenic rape plants with low or modified oil content, diversion of metabolism to alternative storage compounds, e.g. starch, protein or engineered polymers, or production of plants with enhanced oil content. The DNA may also be used as a probe to obtain similar genes from other plants. The transit peptide may be used to direct other proteins to leaf
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Key
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New isolated rape beta-ketoreductase DNA - used to with lower or higher oil contents or with altered c
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N-PSDB; AAQ99305.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-JUL-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (ZENE ) ZENECA LTD
270
                                  236
                                                                  238
                                                                                                                                      178
                                                                                                                                                                      120
                                                                                                                                                                                                         126
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                                                                                                                                                                                                       tfggdvskeadveammkta-idawgtidvvvnn--agi----trdtllirmkksgwdev 177
                                                                                                                                                                                                                                                                                           AAP-MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCV 59
                                                                                                                                                                     NNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCA 178
                                                                                                                                                                                                                                         PVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDI 119
                                                                                                                                                                                                                                                                             avpkvespvvvvtgasrgigkaialslgkagckvlvnyarsakeaeevskgieaygggai 125
                                VVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG
                                                                regasrninvnvvcpgfiasdmtaklgedmek----
                                                                                                HELRRHGVSCVSLWPGIVQTEL --- LKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC 235
                                                                                                                                    idln1tgvf1ctqaatkimmkkrkgriiniasvvg1ignigqanyaaakagvigfsktaa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Elborough
                                                                                                                                                                                                                                                                                                                                                                                                                                     315 AA;
                                                                                                                                                                                                                                                                                                                                               Conservative
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1..55
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                                                                                                                                                                                                                                                                                                                                               13.7%; Score 222.5; DB 17; 25.7%; Pred. No. 7.9e-15; tive 50; Mismatches 108;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               "Transit peptide"
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 304
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밁 Ş 문 Š 문 ş Query Match Best Local S Matches 75 The sequence corresponds to a rape seed beta-ketoreductase encoded by a cDNA insert in plasmid pJRS10.1 in Escherichia coli XLI-Blue. A plastid stroma targeting transit peptide is present. DNA encoding the protein may be inserted in a vector or expression cassette in sense or antisense orientation for expression in an cissed plant, e.g. for production of transgenic rape plants with low or modified oil content, diversion of metabolism to alternative storage compounds, e.g. starch, protein or engineered polymers, or production of plants with enhanced oil content. The DNA may also production of plants with enhanced oil content. Rape; seed; beta-ketoacyl-ACP-ketoreductase; beta-ketoreductase; plasmid pJRS10.1; cDNA library; embryo; Escherichia coli; vector; plastid; stroma; transit peptide; cassette; antisense; oilseed; transgenic plant; crop improvement; lipid; metabolic engineering; polymer; rapeseed oil. Claim 1; Page 15; 29pp; WPI; 1996-105914/11. N-PSDB; AAQ99304. 01-FEB-1996 Key Brassica napus. Sequence plastids be used as a probe to obtain similar transit peptide may be used to direct New isolated rape beta-ketoreductase DNA - used to develop plants with lower or higher oil contents or with altered oil compsn. Chase D, (ZENE ) ZENECA LTD 20-JUL-1994; 17-JUL-1995; WO9602652-A2 Peptide Rape seed beta-ketoacyl-ACP-ketoreductase. 236 VVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG 287 178 126 tfggdvskeadveammkta-idawgtidvvvnn--agi----trdtllirmkksqwdev 238 regasrninvnvvcpgfiasdmtaklgedmek-179 120 60 66 Local Similarity mes 75; Conserv N NNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCA PVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMMDDI 119 avpkvespvvvvtgasrgigkaialslgkagckvlvnyarsakeaeevskqieaygggai 125 AAP-MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCV 59 idlnltgvflctqaatkimmkkrkgriiniasvvglignigqanyaaakagvigfsktaa HELRRHGVSCVSLWPGIVQTEL---LKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC Elborough 315 AA; Conservative 94GB-0014622 95WO-GB01678 /note- "Transit peptide" Location/Qualifiers be used to direct other proteins to seed ~ 13.7%; Score 222.5; DB 17; Length 315; 25.7%; Pred. No. 7.9e-15; tive 50; Mismatches 108; Indels 59; English. Fentem PA, Slabas AR, genes from other plants. .: .: White A; 59; Gaps 235 237 178 177 9

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> 밁 270 --kilgtiplgrygqpedvag--lveflalspaasyitg 304

Search completed: July 31, 2002, 15:08:52 Job time: 231 sec

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Searched:
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Maximum DB seq length: 200000000
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re greater than or equal to the score of the result being printed,
is derived by analysis of the total score distribution.
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| 169  | 120      | 120      | 89   | 37       | 321                | 280                | 256                | 247                | 247                | 241               | 241                | 315                | 315                | 286                | 261                | 258                | 255                | 248                | 246                | 246                | 246      | 246                | 246           | 246      | 244      | 244        | 241      | 15       | 23         | 18       | 33      | 127     | N                  |
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| 945  | AAM74176 | ABB40547 | 164  | AAG73422 | -                  |                    |                    |                    | AAB03794           |                   |                    |                    |                    |                    |                    |                    |                    |                    |                    | AAU37507           | AAU37210 | AAU36530           | AAU33965      | AAB15707 | AAU34533 | AAY54421 · | AAB70963 | AAB98208 | AAG73480 . | AAG73487 | 73      | 7.34    | w                  |
| poly | bone 1   | ×        | huma |          | Drosophila melanog | Streptomyces colli | Gluconate:NADP+-5- | Pseudomonas aerugi | 3-ketoacyl-ACP red | Candida magnoliae | Putative P. abyssi | Rape seed beta-ket | Rape leaf beta-ket | Pseudomonas aerugi | Drosophila melanog | Bacillus D-arabini | ORFL15 protein inv | Amino acid sequenc | S. aureus NADPH-de | Staphylococcus aur |          | Staphylococcus aur | taphylococcus | taphyl   |          | mino a     | lnosa    | P24 pr   | gene 22    | gene 22- | gene 22 | gene 22 | Human colon cancer |

## ALIGNMENTS

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Short-Chain dehydrogenase; HSCD; enzyme; pyruvate; coenzyme A; human; mitochondria; immune disorder; cancer; leukemia; adenocarcinoma; lymphoma; breast; lung; testis; prostate; brain; Addison's disease; acquired immune deficiency syndrome; asthma; anemia; Crohn's disease; Graves disease; AIDS; gene therapy.

US5928923-A.
27-JUL-1999.
05-FEB-1998; 98US-0019216.

Homo sapiens

PA (INCY-) INCYTE PHARM INC.

KX

PI Corley NC, Lal P;

WPI; 1999-429503/36. N-PSDB; AAX86772.

Nucleic acids encoding human short chain dehydrogenase enzymes

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
vulnerary; antipsoriatic; antiparkinsonian; nootropic; neuroprotective; anticonvulsant; osteopathic; antiarthritic; immunosuppressant; cardiant; immunostimulant; thrombolytic; coagulant; vasotropic; antidiabetic; hypotensive; dermatological; immunosuppressive; antidiaheatic; hypotensive; dermatological; immunosuppressive; antiinflammatory; antifungal; antirheumatic; antithyroid; antiviral; antibacterial; antifungal; antirheumatic; antithyroid; antitanaemic; gene therapy; cancer; proliferative disorder; hypertension; neurodegenerative disorder; osteoarthritis; graft va host disorder.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB42640 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            VPKWIIALYTSKF 313
||||||||||||
| vpkwiialytskf 313
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               maapmngqvcvvtgasrgigrgialqlckagatvyitgrhldtlrvvaqeaqslggqcvp
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313; Conserv
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                                                                                                                                                                                                                                                                                              ORF2404 polypeptide sequence
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                                                                                                                                                                                                                                                                                                                     AAC74446 to AAC77606 encode the proteins given in AAB40237 to AAB4397, which represent the human ORFX open reading frames I to 3161. The ORFX sequences have activities such as: cytostatic; hepatotropic; vulnerary; continuous that it is antiparkinsonian; nootropic; neuroprotective; contemporatinic; anticonvulsant; antiarthritic; immunosuppressant; cimmunostimulant; cardiant; thrombolytic; coagulant; vasotropic; contidiabetic; hypotensive; dermatological; immunosuppressive; contitionatory; antibacterial; antivital; antifungal; antirheumatic; contitionatory; antibacterial; antivital; antifungal; antirheumatic; contitionatory; antibacterial; antivital; antifungal; antirheumatic; contitions associated with an ORFX-associated disorder. The presence of or predisposition to, or preventing or treating conticed; acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, concleic acids can be used to express ORFX proteins in gene therapy vectors. The proteins and nucleic acids may be used to treat cancers, confit vs host disease, cardiovascular disease, diabetes mellitus, collesterol ester storage, systemic lupus crythematosus, severe combined immunodeficiency (SCID), AIDS, viral, collesterial or fungal infection, malaria, autoimmune disorders, asthma, conternal haemoglobinuria, antiinflammatory disease; to enhance consulation; to inhibit thrombosis; and as a contraceptive.
                                                                                                                                                                                                       Query Match
Best Local S
Matches 240
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02-APR-1999;
05-APR-1999;
30-MAR-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel nucleic acids and peptides derived from open reading useful for treating e.g. cancers, proliferative disorders, neurodegenerative disorders and cardiovascular disease -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  bone damage; cartilage damage; antiinflammatory thrombosis; contraceptive.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    cardiovascular disease; diabetes mellitus; hypothyroidism;
cholesterol ester storage; systemic lupus erythematosus; i
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    allergy; aplastic
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     194
                                    194
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                                                                                                                                                                                                                             Local Similarity
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LFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGHYFCSVY 133
                                                                  2000-602362/57.
                                                                                                      GARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAACDKLAADCAHELRRHGVSCVSLWP
                                                                                                                                     lfegvdregggrldvlvnnayagvgtilntrnkafwetpasmwddinnvglrghyfcsvy 133
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; 99US-0127636.
; 99US-0127728.
; 2000US-0540763.
                                                                                                                                                                                                         76.7%;
ilarity 100.0%;
Conservative
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ic anaemia; nocturnal haemoglobinuria;
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                                                                                                                                                                                                                         Score 240; Pred. No.
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                                                                                                                                                                                                           Mismatches
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Best Local
                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                     This invention relates to purified human proteins AAB81047 - AAB81056 which are encoded by CDNA sequences AAF77476 - AAF77485. The invention includes an expression vector which can translate DNA encoding the protein or express it in a cell. Also included is a cell transformed by the vector, and an antibody specific for the protein. The protein can be used for the detection of receptors and ilgands and in the screening for new low molecular weight drugs. The present sequence represents the protein product of the human cDNA clone HP00758.
                                                                                                                                                                                                                                                                                                                                                                                                         Claim 1; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                            Novel protein useful for the detection of a receptor and a ligand, and for screening low molecular weight drugs
                                                                                                                                                                                                                                                                    Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (KAGA-) KAGAKU GIJUTSU SHINKO JIGYODAN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    28-JUL-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             28-JUL-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             JP2001037482-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; HP00758; low molecular weight drug.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Human protein HP01017 amino acid sequence.
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                                                                                                                                                                                              Local 240;
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      254
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                                                                                                                                                              74 LFEQVDREQOGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGHYFCSVY 133
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                                                                                                garlmvpaggglivvisspgslqymfnvpygvgkaacdklaadcahelrrhgvscvslwp
                                                                                                               GARLAYPAGQGLIVVISSPGSLQYMENVPYGYGKAACDKLAADCAHELRRHGYSCYSLWP 193
PSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSGLGWLASYLPSFLRVPKWIIALYTSKF 313
                                                givqtellkehmakeevlqdpvlkqfksafssaettelsgkcvvalatdpnilslsgkvl
                                                            GIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALATDPNILSLSGKVL
                                                                                                                                                 lfeqvdreqqgrldvlvnnayagvqtilntrnkafwetpasmwddinnvglrghyfcsvy 133
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2001-285599/30
                                                                                                                                                                                                               Similarity
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                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                     35pp; Japanese.
                                                                                                                                                                                                                76.7%; Score 240; DB 22; 100.0%; Pred. No. 2.1e-234;
                                                                                                                                                                                                       0,
                                                                                                                                                                                                     Mismatches
                                                                                                                                                                                                    0;
                                                                                                                                                                                                                            Length 313;
                                                                                                                                                                                                     Indels
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                                                                                                                                                                                                   Gaps
                                                                                                   193
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RESULT AAG73423

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CC proliferative disorders, cancer, tumours, footal and developmental CC abnormalities, haematopoietic disorders, diseases of the immune system, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC parkinsons's disease), cognitive disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC cardiovascular disorders, pregnancy-related disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound the comburn, to maintain organs before transplantation, for supporting cell CC culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties. CC antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and cin diagnostic immunoassays e.g., radioimmunoassay or enzyme linked conscribed protein of the invention can be used in the invention can be used in the invention can be used in the combusting symptoms associated with the disorders mentioned above, and considered protein of the invention can be used in the invention can be used in the constant of the invention can be used in the constant of the invention can be used in the constant of the invention can be used in the constant of the invention can be used in the constant of the invention can be used in the constant of the invention can be used in the constant of the invention can be used in the constant of the invention can be used in the invention can be used in the constant of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             inflammation; uevelopmental abnormality; haematopoletic disorder; inflammation; allergy; neurological disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; Alzheimer's disease; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary; binding partner identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encountries are protein fragments. The general protein fragments are general protein fragments.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          N-PSDB;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Page 549; 604pp; English.
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2000US-0221193.
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The genes

Söx

Sequence

162

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Query Match Best Local Similarity

46.0%;

Score 144; DB 22; Pred. No. 1.9e-137;

Length 162;

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AAB95802
ID AAB9
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The present invention describes primer sets for synthesising 5602 full-length cDNAs defined in the specification. Where a primer set comprises: (a) an oligo-dT primer and an oligonucleotide complementary to the complementary strand of a polynucleotide which comprises one of the 5602 nucleotide sequences defined in the specification, where the oligonucleotide comprises at least 15 nucleotides; or (b) a combination of an oligonucleotide comprising a sequence complementary to the complementary strand of a polynucleotide which comprises a 5'-end sequence and an oligonucleotide comprises a 3'-end sequence complementary to the polynucleotide which comprises a 3'-end sequence where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide which comprises a 1'-end sequence, where the oligonucleotide comprises at least 15 nucleotides and the combination of the 5'-end sequence/3'-end sequence is selected from those defined in
                                                                                                                                                                                                                                                                                                                                                                                 29-JUL-1999;
27-AUG-1999;
11-JAN-2000;
02-MAY-2000;
09-JUN-2000;
                                                                                                                                                                                      Claim 8;
                                                                                                                                                                                                               Primer sets for synthesizing polynuc full-length cDNAs defined in the spe and/or diagnosis of the abnormality full-length cDNAs
                                                                                                                                                                                                                                                                                                                                040
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                                                                                                                                                                                                                                                                                                                Ishii S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EP1074617-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; primer;
                                                                                                                                                                                                                                                                                                                                                       (HELI:) HELIX RES INST.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  28-JUL-2000;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human protein sequence SEQ ID NO:18783.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAB95802;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAB95802 standard;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cdklaadcahelrrhgvscvslwpgivqtellkehmakeevlqdpvlkqfksafssaett 78
                                                                                                                                                                                                                                                                                                                          Isogai T,
                                                                                                                                                                                      SEQ
                                                                                                                                                                                                                                                                                                              Sugiyama T,
                                                                                                                                                                                                                                                                                                                                                                                99JP-0248036.
99JP-0300253.
2000JP-0118776.
2000JP-0183767.
2000JP-0241899.
                                                                                                                                                                                      ID 18783;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      detection; diagnosis; antisense therapy; gene therapy.
                                                                                                                                                                                                                                                                                                             Nishikawa T,
T, Wakamatsu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Protein; 303
                                                                                                                                                                                2537pp + CD ROM;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0
                                                                                                                                                                                                                                       polynucleotides, particularly the 5602 the specification, and for the detecti
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                                                                                                                                                                                                                                                                                                          Hayashi K,
A, Nagai K,
                                                                                                                                                                                                                            ę,
                                                                                                                                                                                                                            the
                                                                                                                                                                                  English.
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C, Orsuki
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                                                                                                                                                                                                                                                                                                                         Yamamoto J;
combination of defined in
                                                                                                                                                                                                                       detection by the
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RESULT
AAG73485
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Best Local S
Matches 65
                                                                                                                                                                                                                                                                                                                                                                     Parkinson's disease; cognitive disorder; schizophrenia; asthma skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; skin disorder; psoriasis; sepsis; diabetes; kidney disorder; anglogenic disorder; kidney disorder; timour
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  the specification. The primer sets can be used in antisense therapy and in gene therapy. The primers are useful for synthesising polynucleotides, particularly full-length cDNAs. The primers are also useful for the detection and/or diagnosis of the abnormality of the proteins encoded by the full-length cDNAs. The primers allow obtaining of the full-length cDNAs easily without any specialised methods. AAH03166 to AAH13628 and AAH13633 to AAH18742 represent human cDNA sequences; AAB92446 to AAB95893 represent human amino acid sequences; and AAH13632 to AAH13632 represent oligonucleotides, all of which are used in the exemplification
                                                                                                                                                                                  12-NOV-1999;
27-JUL-2000;
                                                                                                                                                                                                                        08-NOV-2000;
                                                                                                                                                                                                                                                                                                                            binding partner
                                                                                                                                                                                                                                                                                                                                       gastrointestinal disorder; pregnancy-related disorder; tumour;
endocrine disorder; infection; wound healing; vulnerary;
cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Human; secreted protein; proliferative disorder; cancer;
foetal abnormality; developmental abnormality; haematopo
                                                                                                      WPI; 2001-329066/34.
                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                    Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                  foetal abnormality; developmental abnormality; haematopoietic diso
immune system disorder; AIDS; autoimmune disease; rheumatoid arthr
inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-AUG-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              standard;
                                                                                                                              Komatsoulis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   22-encoded secreted
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               65
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   20.8%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                99US-0164735.
2000US-0221193.
                                                                                                                                                                                                                        2000WO-US30653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (first entry)
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                                                                                                                                                                                                                                                                                                                            identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Protein;
                                                                                                                             GA,
                                                                                                                             Birse
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 65; DB; Pred. No. 3.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  protein fragment,
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BB
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                                                                                                                             Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                      ia; asthma;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NO:260
                                                                                                                                                                                                                                                                                                                                                                                                                                                          chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
                                                                                                                                                                                                                                                                                                                                                                                                                              c disorder;
arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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0

AAH32522-AAH32627 represent cDNAs corresponding to 35

human secreted

Disclosure;

Page 47;

604pp;

English

Nucleic acids encoding 35 human secreted po preventing, diagnosing and/or treating e.g. disease and diabetic retinopathy -

polypeptides, useful g. cancers, Parkinson

s, useful for Parkinson's

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AIDS, autoimmune diseases (e.g., rheumatoid arthritis), inflammation, allergies, neurological disorders (e.g., Alzheumer's disease, CParkinsons's disease), cognitive disorders, schizophrenia, asthma, compared the schizophrenia asthma, compared the schizophrenia, and infections. The proteins can also be used to aid wound compared the schizophrenia, to prevent skin aging due to compare it schizophrenia, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used compared the specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and companied in the secreted protein fragment referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local s
Matches 49
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                73483
                                                                                                                                                                                                                                                                Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; ALDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimmer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; sgastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary;
12-NOV-1999;
27-JUL-2000;
                                                             08-NOV-2000;
                                                                                                                                                                                                                                                  endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system, alto annotation and diseases of the immune system.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human gene 22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAG73483 standard; Protein; 122 AA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein genes, and AAG73346-AAG73448 represent the proteins they encode AAG73449-AAG73519 represent human secreted protein fragments. The genes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ب
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 Similarity
49; Conserv
                                                                                                                                                                                                                                     partner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       68 AA;
99US-0164735.
2000US-0221193.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                             2000WO-US30653.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.7%; Score 49;
100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 22; 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQ ID NO:258
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ARESULT
AAG73481
ID AAG7
XX
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DT 10-A
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KW Huma
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CC AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted CC protein genes, and AAG73346-AAG73448 represent the proteins they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, CC treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the CC amount of the new protein in a sample or by determining the presence of CC mutations in the new genes. Specific uses are described for each of the C2 genes, based on the tissues in which they are most highly expressed, CC and include developing products for the diagnosis or treatment of C2 genes, based on the tissues in which they are most highly expressed, CC annualities, haematopoietic disorders, diseases of the immune system, CC alpropriative disorders, schizophrenia, asthma, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC antionascular disorders, anglogenic disorders, schizophrenia, asthma, CC cardiovascular disorders, anglogenic disorders, kidney disorders, gastrointestinal disorders, anglogenic disorders, kidney disorders, endocrine CC disorders, and infections. The proteins can also be used to aid wound the healing and epithelial cell proliferation, to prevent skin aging due to culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chenotaxis, and can be used as a food additive or preservative to modify storage properties.

CC antibodies specific for a protein of the invention can be used in disgnostic immunoassays e.g., radioimmunoassay or enzyme linked cindunoscophent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 49; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                        10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG73481;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAG73481 standard; Protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          170 CDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQ
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                                                                                                                                                                                                                                                                                                                            gene
                                                                                                                                                                                                                                                                                                                            22-encoded secreted protein fragment,
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100.0%; Pred. No. 2.
tive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                            NO: 256
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immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; AIDs-Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder.

Human; secreted protein; proliferative disorder; foetal abnormality; developmental abnormality; has

cancer; SEQ

chromosome 14;

ij

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Human

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RESULT
AAG73479
                                                                                                                                                                                                                                            CC protein genes, and AAG73346-AAG73448 represent the proteins they encode. CC AAG73449-AAG73519 represent human secreted protein fragments. The genes CC and their corresponding secreted proteins are useful for preventing, cc treating or ameliorating medical conditions, e.g., by protein or gene CC therapy. Pathological conditions can be diagnosed by determining the cc amount of the new genes specific uses are described for each of the CC amount of the new genes specific uses are described for each of the CC and include developing products for the diagnosis or treatment of CC and include developing products for the diagnosis or treatment of CC and include developing products for the diagnosis or treatment of CC allergies, neurological disorders, classes of the immune system, and include diseases (e.g., rheumatoid arthritis), inflammation, CC allergies, neurological disorders, classes of the immune system, cc allergies, neurological disorders, schizophrenia, asthma, CC skin disorders (e.g., psoriasis), sepsis, diabetes, atherosclerosis, CC parkinsons's disease), cognitive disorders, schizophrenia, asthma, CC sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their CC cognate ligands or binding partners, and in chemotaxis, and can be used to ald mumosorbent assay (ELISA). The present sequence represents a human cCC allerylating symptoms associated with the disorders mentioned above, and communoassays e.g., radioimmunoassay or enzyme linked cCC immunoassays (ELISA). The present sequence represents a human cCC immunoassay (ELISA). The present sequence represents a human cCC immunoassay (ELISA). The present sequence represents a human cCC immunoassay (ELISA). The present sequence represents a human cCC immunoassay or the protein in the discorder content of the invention.
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                                                                                                                                                                    Query Match
Best Local
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                                                                                                     242 DPNILSLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSV 281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive; binding partner identification.
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27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                Similarity
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                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Page 47; 604pp; English.
                                                                                                                                                                12.8%;
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                                                                                                                                                              Score 40;
Pred. No.
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                                                                                                                                              Mismatches
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hes 0;
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AAG73479 standard; Protein; 127

Sequence

127

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cc and their corresponding secreted proteins are useful for preventing, ct treating or ameliorating medical conditions, e.g., by protein or gene ct therapy. Pathological conditions can be diagnosed by determining the camount of the new protein in a sample or by determining the presence of cc amount of the new genes. Specific uses are described for each of the cs 2 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of cc proliferative disorders, cancer, tumours, foetal and developmental can abnormalities, haematopoietic disorders, diseases of the immune system, altergies, neurological disorders (e.g., Alzheimer's disease, cancer stumours, foetal and developmental cc allergies, neurological disorders (e.g., Alzheimer's disease, cc ardiovascular disorders, cognitive disorders, schizophrenia, asthma, cc ardiovascular disorders, programs, schizophrenia, asthma, cc ardiovascular disorders, pregnancy-related disorders, endocrine cd disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used to Althodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., radioimmunoassay or enzyme linked cl immunoaschent assay (ELISA). The present sequence represents a human cc secreted protein fragment referred to in the discrets a the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAH32522-AAH32627 represent cDNAs corresponding to protein genes, and AAG73346-AAG73448 represent the AAG73449-AAG73519 represent human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic acids encoding 35 human secreted preventing, diagnosing and/or treating e. disease and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Page 47; 604pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (HUMA-) HUMAN GENOME SCI INC
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27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             secreted protein; proliferative disorder;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            polypeptides, useful for g. cancers, Parkinson's
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disorder; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    r; cancer; chromosome 14; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQ ID NO:254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               35 human secreted proteins they encode fragments. The genes
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Query Match Best Local :

12.8%;

Score 40; Pred. No.

DB 22; 3e-32;

Length

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       CC AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted CC protein genes, and AAG73346-AAG73448 represent the protein they encode. CC AAG73449-AAG73519 represent human secreted protein fragments. The genes CC treating or ameliorating medical conditions, e.g., by protein or gene CC treating or ameliorating medical conditions, e.g., by protein or gene CC thrappy. Pathological conditions can be diagnosed by determining the genes, based on the new genes. Specific uses are described for each of the CC amount of the new genes. Specific uses are described for each of the CC amount of the new genes. Specific uses are described for each of the CC and include developing products for the diagnosis or treatment of CC and include developing products for the diagnosis or treatment of CC proliferative disorders, cancer, tumours, foetal and developmental CC abnormalities, haematopoletic disorders, diseases of the immune system, CC allergies, neurological disorders (e.g., Alzhelmer's disease, CC cantiovascular disorders, angiogenic disorders, kidney disorders, atherosolerosis, CC Castrolotestlar disorders, angiogenic disorders, kidney disorders, accorders, kidney disorders, angiogenic disorders, kidney disorders, angiogenic disorders, kidney disorders.
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                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-NOV-2000; 2000WO-US30653
                                                                                                                                                                                                                                                                                                                                                                         disease
                                                                                                                                                                                                                                                                                                                                                                                           preventing,
                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic
                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 2001-329066/34
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (HUMA-) HUMAN GENOME SCI INC
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27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  , MS
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40; Conserv
                                                                                                                                                                                                                                                                                                                                                                       acids encoding 35 human secreted polypeptides, useful for ing, diagnosing and/or treating e.g. cancers, Parkinson's and diabetic retinopathy -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    partner identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Komatsoulis
                                                                                                                                                                                                                                                                                                                                    Page 47;
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on; wound healing; vulnerary;
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pregnancy-related disorders,
                                                                                                                                                                                                                                                                                                                                    English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cancer;
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                                        disorders, and infections. The proteins can also be used to aid wound healing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

Antibodies specific for a protein of the invention can be used in alleviating symptoms associated with the disorders mentioned above, and in diagnostic immunoassays e.g., raddolmmunoassay or enzyme linked immunosorbent assay (ELISA). The present sequence represents a human secreted protein fragment referred to in the disclosure of the invention.
Sequence
28
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                                  Matches
                                           Query Match
Best Local
        242 DPNILSLSGKVLPSCDLARRYGLRDVDG 269
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dpnilslsgkvlpscdlarryglrdvdg 28
                                 l Similarity
28; Conser
                                8.9%;
llarity 100.0%;
Conservative
                                 0;
                                          Score 28;
Pred. No.
                                  Mismatches
                                           1.08
                                          .2e-20;
                                                    22;
                                  0
                                                 Length
                                 Indels
                                 0
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Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                         binding
                                                                                                                                                                                                                                                                                                                                                                                                      foetal abnormality; developmental abnormality; haematopoietic disorder; immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                           WO200134628-A1
                                                                                                                                                                                                                                                                                                  Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                        Human; secreted protein; proliferative disorder; cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG73488 standard; peptide; 24
                                                                                                                                                                                                                                                                                                                         partner identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     B
                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                日
                                                                                                                                                                                                                                                                                                                                                                                                                                                                NO:263
                                                                                                                                                                                                                                                                                                                                                                                                                                         chromosome 14;
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AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73448 represent the proteins they encode AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing,

Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy -

WPI; 2001-329066/34

Disclosure;

Page 47;

604pp;

English

12-NOV-1999; 27-JUL-2000; 08-NOV-2000;

2000US-0221193 GENOME SCI INC

9908-0164735

2000WO-US30653.

(HUMA-) HUMAN

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Komatsoulis

GA,

Birse CE,

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Moore

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CC mutations in the new protein in a sample or by determining the CC mutations in the new genes. Specific uses are described for each of the CC 2 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of CC and include developing products for the diagnosis or treatment of CC abnormalities, haematopoietic disorders, diseases of the immune system, allergies, neurological disorders, diseases of the immune system, CC allergies, neurological disorders (e.g., Alzheimer's disease, CC allergies, neurological disorders, e.g., Alzheimer's disease, cognitive disorders, schizophrenia, asthma, CC exidovascular disorders, anglogenic disorders, atherosclerosis, CC skin disorders (e.g., psoriasis), sepsis, disbetes, atherosclerosis, CC disorders, and infections. The proteins can also be used to aid wound CC culture of primary tissues, to regenerate tissues, to identify their CC as a food additive or preservative to modify storage properties. CC antibodies specific for a protein of the invention can be used in diagnostic immunoassays e.g., raddoimmunoassay or enzyme linked immunoassay (ELISA). The present sequence represents a himman cc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
Claim 11; Page 6490-6491; 9803pp; English.
                                                                                   Nucleic acids encoding 4277 human useful for preventing, diagnosing
                                                                                                                                                                                                                                              WPI; 2001-235357/24.
N-PSDB; AAH33358.
                                                                                                                                                                                                                                                                                                                                                                                  Ruben
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 29-SEP-1999;
03-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      28-SEP-2000; 2000WO-US26524.
                                                                                                                                                                                                                                                                                                                                                                                                                                                (HUMA-) HUMAN GENOME
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO200122920-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                05-APR-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; colon cancer; colon cancer antigen; diagnosis; detection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human colon cancer antigen protein SEQ ID NO:4691.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAG73927 standard; Protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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                                                                                                                                                                                                                                                                                                                                                                             , MS
                                                                                                                                                                                                                                                                                                                                                                Barash SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           or amellorating medical conditions, e.g., by protein or gene Pathological conditions can be diagnosed by determining the the new protein in a sample or by determining the presence (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             24 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               990S-0157137.
990S-0163280.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    100.08; **
                                                                                                                                                                                                                                                                                                                                                                                                                                                SCI INC.
                                                                                                                                                                                                                                                                                                                                                            Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Score 24; Pred. No.
                                                         colon cancer-associated polypeptides,
and/or treating colorectal cancers -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       B
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                                                                                                                                                                                                                                                                                                                                                   Rosen CA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                DB 22;
1.1e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            disclosure of the invention
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 24;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
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Nucleic acids encoding 35 human secreted polypeptides, useful for

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Best Local
                                                                                                                                                                                        12-NOV-1999;
27-JUL-2000;
                                WPI; 2001-329066/34.
                                                                                             Ruben
                                                                                                                                                                                                                                                          08-NOV-2000; 2000WO-US30653
                                                                                                                                (HUMA-) HUMAN GENOME SCI INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; anglogenic disorder; kidney disorder disorder; anglogenic disorder; kidney disorder diso
                                                                                                                                                                                                                                                                                                                                                                             WO200134628-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   endocrine disorder; infection; wound hea cell culture; chemotaxis; food additive;
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           immune system disorder; AlDS; autroimmune disease; rheumatoid arthritis; latinson's disease; cognitive disorder; Alzheimer's disease; parkinson's disease; cognitive disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human gene 22-encoded secreted protein fragment,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Human; secreted protein; proliferative disorder; cancer; chromosome foetal abnormality; developmental abnormality; haematopoietic disord
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG73486;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAG73486 standard; Protein; 127
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    expression. For example, N and P may be used to treat disorders associated with decreased expression by rectifying mutations or deletions in a patient's genome that affect the activity of P by expressing inactive proteins or to supplement the patients own production of P. Additionally, N may be used to produce the colon cancer-associated Ps, by inserting the nucleic acids into a host cell and culturing the cell and treatment of colorectal carcinomas and cancers. AAH37196 to AAH37204 and AAB77789 represent sequences used in the exemplification of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            N.B. Pages 666 to 682 and page 7053 of the sequence listing were missing at time of publication, meaning no sequences are present SEQ ID NO:1027 to 1052, 7921 and 7922.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      218 QFKSAFSSAETTELSGKCVVALAT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       cancer associated nucleic acid molecules (N) and proteins (P), where the proteins are collectively known as colon cancer antigens. The color cherapy and vaccine production. N and p may be used in gene diagnosis and treatment of diseases associated with inappropriate P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88 qfksafssaettelsgkcvvalat 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human
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                                                                                             NS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           partner
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24; Conservative
                                                                                Komatsoulis
                                                                                                                                                                                  99US-0164735.
2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   cognitive disorder; schizophrenia; asthma;
                                                                                  GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              100.0%;
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                                                                          Birse CE,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           pregnancy-related
on; wound healing;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 24; Pred. No.
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                                                                     Moore
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     kidney disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NO:261
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RESULT 14
AAG73484
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      amount of the new protein in a sample or by determining the presence of mutations in the new genes. Specific uses are described for each of the 52 genes, based on the tissues in which they are most highly expressed, and include developing products for the diagnosis or treatment of proliferative disorders, cancer, tumours, foetal and developmental abnormalities, haematopoietic disorders, diseases of the immune system,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins they encode AAG73449-AAG73519 represent human secreted protein fragments. The genes
                                                                                                                            yastrointestinal disorder; pregnancy-related disorder; endocrine disorder; infection; wound healing; vulnerary; cell culture; chemotaxis; food additive;
                                                                                                                                                                                Parkinson's disease; cognitive disorder; schizophrenia; asthma; skin disorder; psoriasis; sepsis; diabetes; atherosclerosis; cardiovascular disorder; angiogenic disorder; kidney disorder; gastrointestinal disorder; pregnancy-related disorder; tumour;
                   WO200134628-A1
                                                                                                                                                                                                                                                                                                                                                         Human;
                                                                                                                                                                                                                                                                                                                                                                                               Human gene 22-encoded secreted protein fragment, SEQ ID NO:259.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   10-AUG-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAG73484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAG73484 standard; peptide; 33
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      treating or ameliorating medical conditions, e.g., by protein or gene therapy. Pathological conditions can be diagnosed by determining the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Disclosure; Page 47;
                                                                                                                                                                                                                                                                       Immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis;
inflammation; allergy; neurological disorder; Alzheimer's disease;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        218 QFKSAFSSAETTELSGKCVVALAT 241
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   their corresponding secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 qfksafssaettelsgkcvvalat 111
                                                                                                                                                                                                                                                                                                                         secreted protein; proliferative disorder; cancer; chromosome 14; abnormality; developmental abnormality; haematopoletic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                               partner identification
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     127
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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100.0%; Pred. No.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             DB 22;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4.8e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length 127;
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AAG73487
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CC cardiovas in the tissues in which they are most highly expressed, cc and include developing products for the diagnosis or treatment of cc proliferative disorders, cancer, tumours, foetal and developmental cc abnormalities, haematopoietic disorders, diseases of the immune system, cc allergies, neurological disorders (e.g., rheumatoid arthritis), inflammation, cc allergies, neurological disorders (e.g., Alzheimer's disease, captive disorders, schizophrenia, asthma, cc allergies, neurological disorders, schizophrenia, asthma, cc ardiovascular disorders, angiogenic disorders, kidney disorders, cc cardiovascular disorders, angiogenic disorders, kidney disorders, cc cardiovascular disorders, pregnancy related disorders, andocrine cc disorders, and infections. The proteins can also be used to aid wound chealing and epithelial cell proliferation, to prevent skin aging due to sunburn, to maintain organs before transplantation, for supporting cell cc culture of primary tissues, to regenerate tissues, to identify their cognate ligands or binding partners, and in chemotaxis, and can be used as a food additive or preservative to modify storage properties.

CC Antibodies specific for a protein of the invention can be used in a leviating symptoms associated with the disorders mentioned above, and in alleviating symptoms associated with the disorders mentioned above, and in adance of immunoaceave of a radioimmunoaceave mentioned above, and in adance of immunoaceave and are disorders mentioned above, and consider the disorders mentioned above.
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Best Local S
Matches 20
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Human; secreted protein; proliferative disorder; cancer; chromosome 14; foetal abnormality; developmental abnormality; haematopoietic disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAH32522-AAH32627 represent cDNAs corresponding to 35 human secreted protein genes, and AAG73346-AAG73448 represent the proteins: they encode. AAG73449-AAG73519 represent human secreted protein fragments. The genes and their corresponding secreted proteins are useful for preventing,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             preventing, diagnosing and/or treating disease and diabetic retinopathy -
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27-JUL-2000;
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                                                                                   Human gene 22-encoded secreted protein fragment,
                                                                                                                                          10-AUG-2001 (first entry)
                                                                                                                                                                                                    AAG73487;
                                                                                                                                                                                                                                                     AAG73487 standard; peptide;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Page 47; 604pp; English
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Seemes, based on the tissues in which they are mescribed for each of the composition of the disorders, cancer, tumours, foetal and developmental expressed, altorimume diseases (e.g., rheumatoid arthritis), inflammation, comparison of the immune system, and can be used in disgnostic immune system of the immune system of the invention can be used in comparison of the immune system, comparison of the invention of the invention of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and their corresponding secreted proteins are useful for preventing, treating or ameliorating medical conditions e.g., by protein or gene amount of the new protein in a sample or by determining the mutations in the new genes. Specific uses are described for each of the formance hash on the tiegness in which they are most highly each of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAH32522-AAH32627 represent cDNAs corresponding to AAG73449-AAG73519 represent human secreted protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Nucleic acids encoding 35 human secreted polypeptides, useful for preventing, diagnosing and/or treating e.g. cancers, Parkinson's disease and diabetic retinopathy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (HUMA-) HUMAN GENOME SCI INC.
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27-JUL-2000; 2000US-0221193.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          immune system disorder; AIDS; autoimmune disease; rheumatoid arthritis; inflammation; allergy; neurological disorder; Alzheimer's disease; Parkinson's disease; cognitive disorder; schizophrenia; asthma;
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Query Match Best Local Similarity Matches 18; Conserv

ilarity 100.0%; Score 18; Conservative 0; Mismatc

Mismatches

DB 22; le-10;

22; Length 18;

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Gaps

Search completed: July 31, 2002, 15:13:33 Job time: 232 sec

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Scoring table:
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1795.934 Million cell updates/sec
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Q99104
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Q94FR7
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Q99104 mus musculu
Q99118 mus musculu
Q9n538 caenorhabdi
Q16764 caenorhabdi
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054118 streptomyce
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Q96b59 homo sapien
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                                                              Q9kfr7 bacillus ha
Q98ge0 rhizobium 1
                       Q912r7 pseudomonas
Q92ax2 listeria in
mycobacteri
bacillus su
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SIQUENCE FROM N.A.

TISSUB-TESTIS;

OSHIMA A., Takahashi-Fujii A., Tanase T., Imose N., Takeuchi K.

Arita M., Musashino K., Yuuki H., Hara H., Suzuki Y., Hata H.,

Arita M., Misuno S., Morinaga M., Kawamura M., Sugiyama T.,

Irie R., Otsuki T., Sato H., Nishikawa T., Sugiyama A., Kawakar

Nagai K., Isogai T., Sugano S.;

"NEDO human cDNA sequencing project.";

Submitted (OCT-2001) to the EMEL/GenBank/DDBJ databases.

EMBL; AKOS8159; BAB71694.1; ".
                                                                                                                                                                                                                                                                                                                                                                                               Q96LJ7 PRELIMINARY; PRT; 313 AA.
Q96LJ7;
Q1-DEC-2001 (TrEMBLrel. 19, Created)
Q1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
Q1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
CDNA FLJ25430 FIS, CLONE TST06262.
Homo sapiens (Human)
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
NCBI_TaxID=9606;
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Result No.

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| 14.                |            | 216                | 216    | 216.5              |                    | 218    | •                  | 220.5              | N      | N      | •      | •                  |                    | •                  | •                  | •      | •      | 227    | 227.5  | 7          | 232   | 34         | 234.5  | 239    | 241    | 243                | 247      | 247                |
|                    |            |                    |        |                    |                    |        |                    | •                  |        | •      | •      |                    | •                  |                    |                    |        |        | 14.0   |        |            |       | •          | 14.4   | •      | •      | 5                  | 'n       | Ġ                  |
| 248                | 246        | 257                | 246    | 278                | 254                | 251    | 374                | 328                | 254    | 254    | 320    | 315                | 273                | 271                | 258                | 255    | 272    | 254    | 270    | 257        | 268   | 253        | 247    | 261    | 249    | 266                | 266      | 249                |
| 16                 | 16         | 16                 | 16     | 16                 | N                  | 16     | 16                 | 10                 | 10     | G      | 10     | 10                 | N                  | N                  | 16                 | N      | 10     | ഗ      | 10     | G          | 17    | N          | 16     | 10     | 16     |                    |          |                    |
| Q97FV0             | Q99QK7     | Q987C7             | Q9KA03 | Q9A3M7             | Q9RH24             | Q98FG6 | Q989M0             | Q93X67             | Q949M2 | Q95PA3 | Q93X62 | Q949M3             | Q9F5J1             | 032336             | Q92TX5             | Q9APX4 | Q9SQR2 | Q95PA6 | Q9SQR4 | Q9VNF3     | 9NTH6 | Q9K3Y7     | Q92AK1 | Q9FK50 | Q97DA6 | Q9HWN3             | Q03906   | Q9KEB5             |
| Q97fv0 clostridium | staphyloco | Q987c7 rhizobium 1 |        | Q9a3m7 caulobacter | Q9rh24 zymomonas m |        | Q989m0 rhizobium 1 | Q93x67 brassica na | brass  |        |        | Q949m3 brassica na | Q9f5jl streptomyce | O32336 clostridium | Q92tx5 rhizobium m |        | 2 arab | 0      | •      | drosophile |       | streptomyc | _      |        |        | Q9hwn3 pseudomonas | ø        | Q9keb5 bacillus ha |

Searched:

Sequence:

Title:

Maximum Minimum

Database

Run on:

July 31,

OM protein -

protein search, using sw model

GenCore version 4.5 Copyright (c) 1993 - 2000 Com

Compugen.Ltd.

### ALIGNMENTS

Takeuchi K.,

A., Kawakami

0, Gaps

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Query Match
Best Local Similarity 99.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Strausberg R.;
Submitted (OCT-2001) to the EMBL/GenBank/DDBJ,databases.
EMBL; BC015943; AAH15943.1;
Hypothetical protein.
SEQUENCE 313 AA; 33881 MW; EDOD252724E38776 CRC64;
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Q96B59;
PRELIMINARY;
PRT; 313 AA.

Q96B59;
Q1-DEC-2001 (TremBLrel. 19, Created)
Q1-DEC-2001 (TremBLrel. 19, Last sequence update)
Q1-DEC-2001 (TremBLrel. 19, Last annotation update)
HYPOTHETICAL 33.9 KDA PROTEIN.
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Bukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Primates;
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301 VPKWIIALYTSKF 313
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                                                                                                                                                                                                                                                                                                                                                                                                   NVGLRGHYFCSVYGARLMVPAGOGLIVVISSPGSLQYMFNVPYGVGKAACDKLAADCAHE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MAAPMNGQACVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (TrEMBLrel. 19, (TrEMBLrel. 19,
                                                                                        PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    99.5%;
                 Created)
Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Craniata; Vertebrata; Euteleostomi;
Catarrhini; Hominidae; Homo.
                                                                                  313
                                                                              A.
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                                                                                                                                                                                                                                                                                                                                                              099L04;
01-JUN-2001 (TrEMBLrel. 17, C;
01-JUN-2001 (TrEMBLrel. 17, L;
01-DEC-2001 (TrEMBLrel. 19, L;
RIKEN CDNA 1110029G07 GENE.
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                           EMBL; BC003930; AAH03930.1; MGD; MGI:1915960; 1110029G07Rik. InterPro; IPR002198; ADH_Short, Pfam; pF00106; adh_Short; 1. Oxidoreductase.
                                                                                                             Submitted (FEB-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                        Strausberg R.;
                                                                                                                                                                                                                 TISSUE
                                                                                                                                                                                                                                                                                        Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata;
Mammalla; Eutheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                   TISSUE-MAMMARY TUMOR. WAP-TGF ALPHA MODEL. 7 MONTHS
                                                                                                                                                                                                                                                                                NCBI_TaxID-10090;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Matches
                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                        1110029G07RIK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Q99L04
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                -241 TDPNILSLSGKVLPSGDLARRYGLRDVDGRPVQDYLSLSSVLSHVSGLGWLASYLPSFLR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   301 VPKWIIALYTSKF 313
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 LRRHGVSCVSTMPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALA 240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
TISSUE-PANCREATIC ADENOCARCINOMA;
Strausberg R.;
Submitted (SEP-2001) to the EMBL/GenBank/DDBJ databases
EMBL; BC014057; AAH14057.1; -
SEQUENCE 313 AA; 33925 MW; 37FA022675C4F076 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            121 NYGLRGHYFCSVYGARLMYÞAGQGLÍVVÍSSÞGSLQYNFNYLYGVGKAACDKLAADCAHE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-DEC-2001 (TremBLrel. 19, Last annot SIMILAR TO RIKEN CONA 1110029G07 GENE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Homo sapiens (Human)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 MAAPMNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                PRELIMINARY;
                   ĀΑ;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
           34005 MW;
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99.48;
                                                                                                                                                                                                                                                                                                                                                                        Last sequence update;
Last annotation update;
                                                                                                                                                                                                                                                                                                                                                                                                                         Created)
60E05BD7911BDC0C CRC64;
                                                                                                                                                                                                                                                                            Craniata; Vertebrata;
Sciurognathi; Muridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 1609; DB 4;
Pred. No. 8.9e-133;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          313
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                                                                                                                                                                                                                                                                              Muridae;
                                                                                                                                                                                                     OLD,
                                                                                                                                                                                                                                                                                         Euteleostom1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 313;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels.
                                                                                                                                                                                                                                                                        Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Euteleostomi; Homo.
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300

240

120

RESULT Q96B59 ID Q9

S 밁 Ş 멍 Ş 밁

241

181 181 121

RESULT Q96CQ5 ID Q9 AC Q9 DT Q1 DT Q1

096CQ5 Q96CQ5; 01-DEC-2001 01-DEC-2001

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301

181

121 121

61 61

Query Match Best Local Similarity

85.7%; 82.4%;

Score 1391; Pred. No. 1.

, DB 11; 1.1e-113;

Length 313; Indels

258;

Conservative

27;

Mismatches

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                                                                                                                                                                         A Rawal J., Shinagawa A., Shibata K., Yoshino M., Itoh M., Ishii Y.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Arakawa T., Hara A., Fukunishi Y., Konno H., Adachi J., Fukuda S.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Nishi K., Kiyosawa H., Kondo S., Yamanaka I.,
A Alzawa K., Izawa M., Olopori T., Bono H., Kasukawa T., Saito R.,
A Kadota K., Matsuda H.A., Ashburner M., Battalov S., Casavant T.,
A Kadota K., Matsuda H.A., Ashburner M., Battalov S., Casavant T.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Kuehl P., Lewis S., Matsuo Y., Nikaido I., Pesole G., Quackenbush J.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Schriml L.M., Staubli F., Suzuki R., Tomita M., Wagner L., Washio T.,
A Sakai K., Okido T., Furuno M., Aono H., Baldarelli R., Barsh G.,
Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Boffelli D., Bojunga N., Carninci P., de Bonaldo M.F.,
A Blake J., Butt C., Fletcher C., Fujita M., Gariboldi M.,
Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Gustincich S., Hill D., Hofmann M., Hume D.A., Kamiya M., Lee N.H.,
A Mordone P., Ring B., Ringwald M., Rodriguez I., Sakamoto N.,
A Sasaki H., Sato R., Schoenbach C., Seya T., Shibata Y., Storch K.-F.,
A Wynshaw-Boris A., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
A Hayashtzaki Y., Storch R., Yoshida K., Hasegawa Y., Kawaji H., Kohtsuki S.,
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O9D148;
O9D148;
O1-JUN-2001 (TrEMBLrel.
O1-JUN-2001 (TrEMBLrel.
O1-DEC-2001 (TrEMBLrel.
1110029G07RIK PROTEIN.
Mature 409:685-690(2001).

EMBL; AK003958; BAB23093.1; -..

MGD; MGI:1915560; 1110029607R1k.

SEQUENCE 313 AA; 34031 MW; 8
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Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STRAIN-C57BL/6J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mus musculus
                                                                                                                           "Functional annotation of a full-length mouse cDNA collection.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-21085660; PubMed-11217851;
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(TrEMBLrel. 17, Last sequence up)
(TrEMBLrel. 19, Last annotation)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (Mouse)
letazoa; Chordata;
ltheria; Rodentia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TISSUE-EMBRYO;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Craniata; Vertebrata; Euteleostomi; Sciurognathi; Muridae; Murinae; Mus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRT;
80E8ECD7910EDC03 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   313
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Query Match Best Local Similarity

84.4%;

Score 1370; DB 11; Pred. No. 7.6e-112;

Length

Query Match Best Local Similarity

43.7%;

Score 710; Pred. No. 5

5e-54;

Length 319;

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"The sequence of C. clegans cosmid Y32H12A.";

"The sequence of C. clegans cosmid Y32H12A.";
                                                                                           "Direct Submission.";
Submitted (JUL-2001) to the EMBL/GenBank/DDBJ databases.
-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                  STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                          Caenorhabditis elegans.
                                                                                                                                                                                                                                                                                                                                                                                                                01-0CT-2000 (TrEMBLrel. 15, Cr. 01-0CT-2000 (TrEMBLrel. 15, La. 01-DEC-2001 (TrEMBLrel. 19, La. HYPOTHETICAL 35.1 KDA PROTEIN.
PRINTS; PRO0080; SDRFAMILY; UNKNOWN 1.
PROSTTE; PS00601; ADH_SHORT; UNKNOWN 1.
Hypothetical protein; Oxidoreductase.
SEQUENCE 319 AA; 35067 MW; F6B5DDAE07EE734E CRC64;
                                              EMBL; AC006733; AAF60486.1; -. HSSP; P50162; IAE1. InterPro; IPR002198; ADH_short.
                                                                                                                                                                                                                                                       "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium."; Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                       STRAIN-BRISTOL N2; MEDLINE-99069613;
                                                                                                                                                                                                                                                                                                                                                      Rhabditidae; Peloderinae; NCBI_TaxID=6239;
                                                                                                                                                                                                                                                                                                                                                                                                       Y32H12A.3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Q9N538;
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                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LRRHGVSYVSLWPRLVQTEMVKEFMAKEDTPEDPLFKKMKPDFSSAESPEMSGKCVVALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | LRRHGVSCVSLWPGIVQTELLKEHWAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAACDKLAADCAHE
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Last seq
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RESULT
OLO 701
OLO 702
OLO 703
OLO 703
OLO 703
OLO 704
OLO 704
OLO 705
             Query Match
Best Local Similarity
Matches 138; Conserv
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                                                                                                                               EMBL; AF016685; AAG24139.1; -
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
Hypothetical protein; Oxidoreductase.
SEQUENCE 323 AA; 35824 MW; 4FE24D30ED39CAE3 CRC64;
                                                                                                                                                                                                                                                                                           "Direct Submission.";
Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
-!- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             O16764;
O1-TAN-1998 (TrEMBLrel. 05, Created)
O1-TAN-1998 (TrEMBLrel. 05, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation updat
HYPOTHETICAL 35.8 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Bradshaw H.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. investigating biology. The C. elegar Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          DDINNYGLRGHYFCSYYGARLMYPAGQGLIVYISSPGSLQYMFNYPYGYGKAACDKLAAD 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GOVCVVTGASRGIGRGIALQLCKAGATVYITGRH-------LDTLRVVAQEAQSLGG
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             Conservative
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  37.9%; Score 615; DB 5; 42.1%; Pred. No. 1.1e-45; Live 58; Mismatches 112;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     cosmid F59E11.";
EMBL/GenBank/DDBJ databases
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elegans Sequencing
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                                                       Length 323;
     Indels
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                                                                                                                                                   RESULT Q23612
ID 3612
AC Q2
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Matches 130
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5 MNGQVCVVTGASRGIGR----GIALQLCKAGATVYITGR---

Indels

36;

Gaps

5

---HLDTLRVVAQ 49

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SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
Nhan M., Leimbac D.;
"The sequence of C. el
Submitted (DEC-1995) t
                                                                                (SDR) FAMILY.

(SDR) FAMILY.

(SDR) FAMILY.

EMBL; U41018; AAA82327.1; -.

InterPro; IPR002198; ADH_Short.

Pfam; PF00106; adh_Short; 1:

PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.

Hypothetical protein; Oxidoreductase.

SEQUENCE 325 AA; 35919 MW; D68C60E9105AE177 CRC64;
                                                                                                                                                                                                                      "Direct Submission.",
Submitted (JUN-2001) to
-1 - SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q23612
Q23612;
Q1-NOV-1996
Q1-NOV-1996
Q1-DEC-2001
                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A. STRAIN-BRISTOL N2; Waterston R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         "Genome sequence of the nematode C. elegans: a pinvestigating biology. The C. elegans Sequencing Science 282:2012-2018(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-BRISTOL N2;
MEDLINE-99069613; PubMed-9851916;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Nemat
Rhabditidae; Peloderinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence up
01-DEC-2001 (TrEMBLrel. 19, Last annotation
HYPOTHETICAL 35.9 KDA PROTEIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Caenorhabditis elegans.
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MGKEEVAKYIPPQIKLPKWVIWQSVNRF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ARMSTDMAVELNPYNVCVVTLIPGPVKTETANRTIIDDAYKMIKENPELEE----FIKGE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TTELSGKCYVALATDPNILSLSGKVLPSCDLARRYGLRDVDGRPV--QDYLSLSSVLSHV
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                                                                                                                                                                                                                                                                                                                                                 . elegans
5) to the
                      35.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nematoda;
                                                                                                                                                                                                              the EMBL/GenBank/DDBJ databases.
TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     oda; Chromadorea;
Caenorhabditis.
                                                                                                                                                                                                                                                                                                                                             cosmid ZK816.";
EMBL/GenBank/DDBJ
Score 583; DB 5; | Pred. No. 6.8e-43; | 5; Mismatches 111;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       323
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                                   Length 325
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                                                  Matches
                                                            Query Match
Best Local
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Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; St
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01-JUN-1998 (TrEMBLrel.
01-JUN-1998 (TrEMBLrel.
01-DEC-2001 (TrEMBLrel.
                                                                                                             SEQUENCE
                                                                                                                        Oxidoreductase.
                                                                                                                              (SDR) FAMILY.
EMBL; ALO21529; CAA16459.1; -.
InterPro; IPR002198; ADH_short.
Pfam; PP00106; adh_short; 1.
                                                                                                                                                                                 Redenbach M., Kieser H.M., Denapaite D.,
Kinashi H., Hopwood D.A.;
Kinashi H., Hopwood D.A.;
"A set of ordered cosmids and a detailed
"A set of ordered cosmids and a detailed
the 8 MD Streptomyces coelicolor A3(2) ch
Mol. Microbiol. 21:77-96(1996).
-1- SIMILARITY: BELONGS TO THE SHORT-CHAI
                                                                                                                                                                                                                                           MEDLINE-97000351; PubMed-8843436; Redenbach M., Kieser H.M., Denapaite D.,
                                                                                                                                                                                                                                                                       STRAIN-A3(2)
                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                    Murphy L., Harris D.;
Submitted (JAN-1998) to
                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A. STRAIN-A3(2);
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                                                                                                                                                                                                                                                                                                            Submitted
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -- FLNGESTEYCGKAVVAIAADPKKKYWNGSTLITTDMGNYYSYTDIDGRIPTNMRQLRG
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                         PMNGQVCVVTGASRGIGRGIALQLCKAGATVYIT------GRHLDTLRVVAQEAQ 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ALDRMSSDMAQELQDTGITVISLWPSAVKTELITNMIETSAGSWGATENKM-----
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ERDPEIWDDINNYGLRNQYYCSYYGTRIMRKNGMKGLIVNISSLGGIMYLFTVAYGVGKM
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                                                              Similarity
                                                                                                                                                                                                                                                                                                                      3(2);
                                                                                                                                                                                                                                                                                                         J., Barrell (JAN-1998)
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                                                                                                             35276 MW;
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19,
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e EMBL/GenBank/DDBJ
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                                                Score 347.5; DB 2
Pred. No. 2.9e-22;
5; Mismatches 102
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                                                                                                             CB8F3D5B218B0EB9 CRC64;
                                                                                                                                                                                    SHORT-CHAIN
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                                                                                                                                                                                                          chromosome.
                                                                                                                                                                                                          genetic and
hromosome.";
                                                                                                                                                                                                                                             Eichner A.,
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                                                                        DB 2;
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                                                                                                                                                                                                                     physical map
                                                 39;
                                                Gaps
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Q9KFR7;
01-OCT-2000
01-OCT-2000
01-DEC-2001
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Bacillus/Staphylococcus
Bacillus/Staphylococcus
Bacillus/Staphylococcus
Bacteria; Firmicutes; Bacteria; Bacter
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Takami H., Nakasone K., Takaki Y., Maeno G., Sasaki R
Fuji F., Hirama C., Nakamura Y., Ogasawara N., Kuhara
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STRAIN=C-125 / JCM 9153;
MEDLINE=20512582; PubMed=11058132;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EMBL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans and genomic sequence comparison with Bacillus subtilis."; Nucleic Acids Res. 28:4317-4331(2000).
-1- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
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                                                                                              171
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PHFVISESPRFVGRAVAALASDPNVSRWNGQSLSSGQLAQAYGFTDLDG
                       SAFSSAETTELSGKCVVALATDPNILSLSGKVLPSCDLARRYGLRDVDG
                                                                                              YYDLAKTSVLRWAWGLAQELQPHECTAVALTPGWMRSEIMLDHFEVTERNWRDATIKE--
                                                                                                                                                                                                                                                                                                                                                 LGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPA 113
                                                                                                                                                                                                                                                                                                                                                                                                     PLIGKVALVAGATRGAGRGIAVELGAAGATVYVTGRTTRERRSEYNRPETIEETAELVTN
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                                                                                                                                                                                                PVWQHSLDDGLRMLRLAIDTHLITSHFALPLLLKS-RGLVVEWTD-GTAEYNREHYRQPL
                                                                                                                                                                                                                                                  SMWDDINNVGLR-----GHYFCSVYGARLMVPAGQGLIVVISSPGSLQY---MFNVP-
                                                                                                                           -YGVGKAACDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM-AKEEVLQDPVLKQFK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AP001508; BAB04129.1; -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94;
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33422 MW; CEl3F300140D55BB
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ús group; Bacillus:
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Last annotation updat
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Pred. No. 5.
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Best Local
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DNA Res. 7:331-338(2000).
EMBL; AP003001; BAB50276.1; ...
InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
OPEWT2;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-MAR-2001 (TrEMBLrel. 16, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
PUTATIVE OXIDOREDUCTASE.
3SC5B7.17C.
Streptomyces coelicolor.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae;
Actinomycetales; Streptomycineae; Streptomycetaceae; Streptomyces.
                                                                                                                                                                                                               Q9EWT2
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STRAIN-WAFF303099;
MEDLINE-21082930; PubMed-11214968;
Kaneko T., Nakamura Y., Sato S., Asamizu E., Kato T., Sasam Watanabe A., Idesawa K., Ishikawa A., Kawashima K., Kimura K.shida Y., Kiyokawa C., Kohara M., Matsumoto M., Matsuno A Mochizuki Y., Nakayama S., Nakazaki N., Shimpo S., Sugimoto Takeuchi C., Yamada M., Tabata S.
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01-0CT-2001 (Trem
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Bacteria; Proteobacteria; alpha su
Phyllobacteriaceae; Mesorhizobium.
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Last sequence update)
Last annotation update)
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Pred. No. 1.6e-21;
3; Mismatches 103;
                                                                                                                                                                                                        PRT;
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Sugimoto M.,
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Best Local
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SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

STRAIN-ARCC 15692 / PAO1;

MEDLINE-20437337; PubMed-10984043;

MEDLINE-20437337; PubMed-10984043;

Stover C.K., Pham X.-Q.T., Erwin A.L., Mizoguchi S.D., Warrener P.,

Hickey M.J., Brinkman F.S.L., Hufnagle W.O., Kowalik D.J., Lagrou M.

Garber R.L., Goltry L., Tolentino E., Westbrock-Wadman S., Yuan Y.,

Brody L.L., Coulter S.N., Folger K.R., Kas A., Larbig K., Lim R.M.,
                                                                                                                                                                                                                                                                                                                   O912R7 PRELIMINARY; PRT; 255 AA.
O912R7;
O1-MAR-2001 (TrEMBLrel. 16, Created)
O1-DEC-2001 (TrEMBLrel. 19, Last sequence update)
O1-DEC-2001 (TrEMBLrel. 19, Last annotation update)
                                                                                                                                                                                                                                            Pseudomonas aeruginosa.
Bacteria; Proteobacteria;
                                                                                                                                                                                                                                                                                                PA1828.
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                                                                                                                                                                                                                                 Pseudomonas
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"A set of ordered cosmids and a detailed genetic a the 8 Mb Streptomyces coelicolor A3(2) chromosome. Mol. Microbiol. 21:77-96(1996).

MBL; AL449216; CAC14941.1;
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Seeger K.J.,
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SEQUENCE FROM N.A.
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PRINTS; PRO0080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
Complete proteome; Oxidoreductase.
Complete proteome; Oxidoreductase.
255 AA; 26919 MW; D60
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      "Comparative genomics of Listeria species."; Science 294:849-852(2001).
EMBL; AL596170; CAC97027.1; -.
Listilist: ITMN1706.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Glaser P., Frangeul L.,
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NCBI_TaxID=1642;
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Saier M.H., Hancock R.E.W., 1
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Lory S., Olson M.V.;
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PRINTS; PROOR80; SDREAMLLI.

PROSITE; PS00061; ADH_SHORT; UNKNOWN_1.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

PROSITE; PS00038; HELIX_LOOP_HELIX; UNKNOWN_1.

Complete proteome; Hypothetical protein; Oxidoreductase.

Complete proteome; 255 AA; 27031 MW; 454692E6FAA253FF CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE-98295987; PubMed-9634230;
Gold S.T., Brosch R., Parkhill J., Garnier T., Churcher C., H
Gordon S.V., Eiglmeier K., Gas S., Barry C.E. III, Tekaia F.,
Badcock K., Basham D., Brown D., Chillingworth T., Connor R.,
Davies R., Devlin K., Feltwell T., Gentles S., Hamlin N., Hol
Davies R., Devlin K., Krogh A., McLean J., Moule S., Murphy
Oliver S., Osborne J., Quail M.A., Rajandream M.A., Rogers J.
Rutter S., Seeger K., Skelton S., Squares S., Squares R.,
Sulston J.E., Taylor K., Whitehead S., Barrell B.G.;
"Deciphering the biology of Mycobacterium tuberculosis from t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Deciphering the biology of Mycobacterium complete genome sequence.";
Nature 393:537-544(1998).
-i- SIMILARITY: BELONGS TO THE SHORT-CHAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Mycobacterium tuberculosis.
Bacteria; Firmicutes; Actinobacteria; Actinobacteridae; Actinomycetales; Corynebacterineae; Mycobacteriaceae; M
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCVPVVC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           17.7%;
                                      16.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         36;
Score 271; DB pred. No. 1e-1 Pred. No. 1e-1 Pred. Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Score 286.5; DB
Pred. No. 4.3e-17
6; Mismatches 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    19026CBBCD0806FF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              206
                                                                                  B
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                                                                                  16;
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                                                                                  255;
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MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64

Matches

Similarity

Conservative

37;

1e-15;

.83

Indels

14;

Gaps

Ş

# GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: July 31, 2002, 15:05:36 ; Search time 17.53 Seconds (without alignments)
1715.685 Million cell updates/sec

Sequence: US-10-006-163-1 1623 1 MAAPMNGQVCVVTGASRGIG...:...YLPSFLRVPKWIIALYTSKF 313

Title: Perfect score:

Scoring table:

BLOSUM62 Gapop 10.0 , Gapext 0.5

Searched:

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Total number of hits satisfying chosen parameters: 283138

283138 seqs, 96089334 residues

Post-processing: Minimum Match 0% .
Maximum Match 100%
Listing first 45 summaries

PIR\_71:\*
1: pir1:\*
2: pir2:\*
3: pir3:\*
4: pir4:\*

Database :

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| 3 3 4 4 4 5 5 5 5 5 6 5 5 6 5 6 5 6 6 6 6 6   | Result<br>No.                  |
|---|--------------------------------|
| 583<br>347.5<br>343.5<br>343.5<br>286.5<br>286.5<br>284.5<br>262<br>254<br>247<br>247<br>247<br>247<br>247<br>247<br>247<br>24  | Score<br>617.5                 |
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| 323<br>323<br>326<br>2248<br>2250<br>2248<br>2250<br>2260<br>2260<br>2260<br>2260<br>2260<br>2260<br>2260   |                                |
| 00000000000000000000000000000000000000  | DB                             |
| 732125<br>732504<br>734594<br>134594<br>1083416<br>AC1657<br>AH1285<br>AH1285<br>2698021<br>883767<br>883767<br>842042<br>883767<br>8432042<br>783120<br>8431672<br>AG1672<br>AG1672<br>AG1672<br>AG1673<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG1674<br>AG167 | ID<br>AE2212                   |
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279 SSVLSHVSGLGWLASYLPSFLRVPKWIIAL 308
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310 PTLRKH----SWL---IPD-IKVP-WSILL 330

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RESULT

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| 44                                       | 422   | 409  |  | 30<br>32<br>34   |
|--|---|--|--|--|
| 210                                      | 210.5   | 213<br>212.5<br>211.5  | 214<br>214<br>213.5  | 216.5<br>216<br>216<br>215<br>214.5<br>214.5   |
| 12.9<br>12.9                             | 13.0<br>13.0<br>12.9  | 13.1   | 13.2<br>13.2   | 13.3<br>13.2<br>13.2   |
| 254<br>251                               | 258<br>247<br>242   | 256<br>281   | 274<br>320<br>275  | 278<br>246<br>247<br>246<br>248  |
| N. N                                     | 2020  | N N N  | NNN  | 22222  |
| AC3256<br>AC0103                         | H75616<br>B83880<br>C86237                                    | AD3235<br>F69400<br>T07698                                     | G83284<br>S22450<br>I40211                                     | E87642<br>C83961<br>S77280<br>B89896<br>B97223   |
| 3-oxoacyl-(acyl-ca<br>2-deoxy-D-gluconat | oxidoreductase, sh<br>3-oxoacyl-(acyl-ca<br>protein Fl4N23.19 | 2-deoxy-D-gluconat<br>2-deoxy-D-gluconat<br>short-chain alcoho | probable short-cha<br>3-oxoacyl-[acyl-ca<br>probable sterol de | short chain dehydr<br>3-oxoacyl-(acyl-ca<br>3-oxoacyl-(acyl-ca<br>3-oxoacyl-(acyl-ca<br>probable 3-ketoacy |

# ALIGNMENTS

| QY 227 ETTELSGKCYVALATDPNILSLSGKVLPSCDLARRYGLRDVDGR-PVQDYLSL 278 | Qy 171 DKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFK-SAFSSA | Qy 111 TPASMWDDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAAC 170 | Qy 51 AQSIGGQCVPVVCDSSQESEVRTIFBQVDREQQGRLDVIVNNAYAGVQTILNTRNKAFWE | Qy 5 MNGQVCVVTGASRGIĞRGIALQLCKAGATVYITGRHLDTLRVVAQE 50 :  :  :  :  :  :  :  :  :     :      :  : | Query Match 38.0%; Score 617.5; DB 2; Length Best Local Similarity 43.0%; Pred. No. 1e-42; Matches 142; Conservative 53; Mismatches 94; Indels | AE2212 hypothetical protein alr3252 [imported] - Anabaena sp. (strain PCC 7120) c;Species: Anabaena sp. A;Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C;Accession: AE2212 R;Raneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Irig Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabat DNA Res. 8, 205-213, 2001 A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium A;Reference number: AB1807; MUID:21595285; PMID:11759840 A;Accession: AE2212 A;Status: preliminary A;Molecule type: DNA A;Residues: 1-339 <kur> A;Cross:references: GB:BA000019; PIDN:BAB74951.1; PID:g17132347; GSPDB:GN00179 A;Experimental source: strain PCC 7120 C;Genetics: A;Gene: alr3252</kur> |
|--|--|---|--|--|--|---|
| GLRDVDGR-PVODYLSL 278  | KEEVLODPVLKOFK-SAFSSA 226  | VVISSPGSLQYMENVPYGVGKAAC 170<br>  | DVLVNNAYAGVQTILNTRNKAEWE 110<br> -                                 | LDTLRVVAQE 50  | DB 2; Length 339;<br>-42; 42; Indels 41; Gaps 12;  | aena sp. (strain PCC 7120)  nonym of Nostoc sp. strain PCC 7120 2001 #text_change 11-Jan-2002  , T.; Sasamoto, S.; Watanabe, A.; Irig. awa, M.; Yamada, M.; Yasuda, M.; Tabat. mentous Nitrogen-fixing Cyanobacterium D:11759840  .1; PID:g17132347; GSPDB:GN00179  |

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A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-325 <NHA>
                                                                                                       A; Introns: 24/1;
                                                                                                                                    A;Cross-references: EMBL:U41018; PIDN:AAA82327.1; CESP:ZK816.
                                                                                                                                                                                                                  A; Reference number:
A; Accession: T29604
                                                                                                                                                                                                                                        submitted to the EMBL Data Library, November 1995 A; Description: The sequence of C. elegans cosmid ZK816.
                                                                                                                                                                                                                                                                                                     hypothetical protein ZK816.5 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 15-Oct-1999
C;Accession: T29604
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                                                                                    ;Gene: CESP:2K816.5
;Introns: 24/1; 111/3; 170/2; 228/3; 280/1
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A;Residues: 1-323 <BRA>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         submitted to the EMBL Data Library, July 1997
A;Description: The sequence of C. elegans cosmid F59E11.
A;Accession: T32125
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hypothetical protein F59E11.2 - Caenorhabditis elegans
C:Species: Caenorhabditis elegans
C:Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change
C:Accession: T32125
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Best Local Similarity
                                    Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TPASMWDDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAAC 170
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42.1%;
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                         Score 583; DB 2;
Pred. No. 6.3e-40;
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Pred. No. 1.5e-42;
            Mismatches
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            111;
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        Indels
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A; Residues: 1-326 <MUR>
A; Cross-references: EMB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    A; Experimental source: strain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Status: preliminary; translated from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       probable oxidoreductase - Streptomyces coelicolor
C;Species: Streptomyces coelicolor
C;Date: 05-Nov-1999 #sequence_revision 05-Nov-1999 #text_change
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                                                                                                                                                                                                                                                                                                           4 PMNGQVCVVTGASRGIGRGIALQLCKAGATVYIT------
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                                                                                             NIYYDLAKNAPIRLAFGLAQELAEYEGTAVAVSPGFLRSEQMLSHFGVSEENWRDAIAQE
                                                                                                                                                      TPLADGLRILELGARSH----VITAALLLP----LLIRSDAPLHVEVTDGTAHSNRRYRE
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                                                                                                                                                                                                                 AAGGTGIAVPTDHLDEAQVRALVERIDREYE-RLDILVNDLWGG-EHLLATSVFGKKSWE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       EAQSLGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFW 109
                                                                                                                                                                                                                                                                                                                                                      99;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ECRKRGGICHVRYVDHSNMDEVEKFFDEVASETDNQLDILVNNAFSAVTKCGSGDTRKFF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LKSKIAIVTGASRGCGRGMLKGVALQLAEAGCTLYITGRAPSKTLSSELTYLPTLEGTAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MNGQVCVVTGASRGIGR----GIALQLCKAGATVYITGR-----
                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL:ALO21529; PIDN:CAA16459.1; GSPDB:GN00070;
ce: strain A3(2)
                                                                                                                                                                                                                                                                                                                                       21.4%; Score 347.5; DB 2; 33.6%; Pred. No. 1e-20; Fr. Mismatches 102;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             B.G.; Rajandream,
                                                                                                                                                                                                                                                                                                        -GRHLDTLRVVAQEAQ
                                                                                                                                                                                                                                                                                                                                                                    Length 326;
                                                                                                                                                                                                                                                                                                                                          Indels
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                                                                                                                                                                                                                                                                                                                                       39;
                                      304
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          05-Nov-1999
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                                                                                                                                                                                                                                                                                                                                    Gaps
                                                                                                251
                                                                                                                                                        191
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                                                                                                                                                                                                                                                                                                                                    11;
```

hypothetical

protein

BH0410

[imported] -

Bacillus

halodurans

(strain C-125)

229 233 122

119

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C; Species: Bacillus
C; Date: 01-Dec-2000
C; Accession: B83701
R; Takami, H.; Nakaso
                                                                                                                                                                                                                                                                                                                                                                ; Lory, S.; Olson, M.V.

Nature 406, 959-964, 2000

A;Title: Complete genome sequence of Pseudomonas aeruginosa PA01, an A;Reference number: A82950; MUID:20437337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C; Accession: D83416
R; Stover, C.K.; Pham, X.Q.;
adman, S.; Yuan, Y.; Brody,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           probable short-chain dehydrogenase PA1828 [imported] - Pseudomonas aeruginosa C:Species: Pseudomonas aeruginosa C:Species: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                RESULT
D83416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A;Molecule type: DNA
A;Residues: 1-302 <5T0>
A;Cross-references: GB:AP001508; GB:BA000004; NID:g10172890;
A;Experimental source: strain C-125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masul, N.; Fuji, F.; Nucleic Acids Res. 28, 4317-4331, 2000
A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A3650; MUID:20512582; PMID:11058132 , A;Accession: B83701
                             밁
                                                            Ş
                                                                                                                                                                                                                                                                    A;Cross-references: GB:AE004609; GB:AE004091; NID:g9947810; PIDN:AAG05217.1; A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                          A; Molecule type: DNA
A; Residues: 1-255 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               밁
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                                                                                                                                                                                                                                                                                                                                                      A;Status:
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                                                                                                                                                                                                        ;Superfamily: ribitol dehydrogenase; short-chain alcohol
                                                                                                                                                                                                                                 ;Gene: PA1828
                                                                                                        Query Match
Best Local Similarity
Matches 87; Conserv
                                                                                                                                                                                                                                                  Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Species: Bacillus halodurans
Date: 01-Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BH0410
                                                                                                                                                                                                                                                                                                                                                    preliminary
                    LDGKIAFVSGASRGIGEAIAKLLAQQGAHVIVSSRKIDGCQAVADAITAEGGKATAIACH 68
                                                            MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SAFSSAETTELSGKCYVALATDPNILSLSGKVLPSCDLARRYGLRDVDG 269
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YYDLAKTSVLRMAWGLAQELQPHECTAVALTPGWMRSEIMLDHFEVTERNWRDATIKE--
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PVWQHSLDDGLRMLRLAIDTHLITSHFALPLLLKS-RGLVVEMTD-GTAEYNREHYRQPL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SMWDDINNVGLR-----GHYFCSYYGARLMVPAGQGLIVVISSPGSLQY---MENVP-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AGGTGIAVPVDHLDPQKVEALVSQIERE-QGKLDVLVNDIWGG-----ELLTEWNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LGGQCVPVVCDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPA 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PLIGKVALVAGATRGAGRGIAVELGAAGATVYVTGRTTRERRSEYNRPETIEETAELVTN 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YGVGKAACDKLAADCAHELRRHGVSCVSLWPGIVQTELLKEHM-AKEEVLQDPVLKQFK 220
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Similarity
                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  21.2%;
                                                                                                                             19.18;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erwin, A.L.; Mizoguchi, S.D.; Warrener, L.L.; Coulter, S.N.; Folger, K.R.; Kas,
                                                                                                        44;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             57;
                                                                                                                       Score 310; DB 2;
Pred. No. 8.3e-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 343.5; DB 2;
Pred. No. 1.9e-20;
7; Mismatches 101;
                                                                                                        Mismatches
                                                                                                                                             Length 255;
                                                                                                        Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length
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                                                                                                                                                                                                    dehydrogenase homology
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     302;
                                                                                                        42;
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                                                                                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Hickey,
Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             10;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  M.J.; BI
K.; Lim,
                                                                                                                                                                                                                                                                                                                                                                                                        pathq
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R;Glaser, r.,
Dominguez-Bernal, G.; Duchaux, ...
D.; Jones, L.M.; Karst, U.
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
A;Authors: Kreft, J.; Kuhn, M.; Kunst, F.; Kurapkat, G.; Madueno, E.; A;Authors: Kreft, J.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; ok, C.; Schlueter, T.; Simoes, N.; Tierrez, A.; Vazquez-Boland, J.A.; A;Title: Comparative genomics of Listeria species.
A;Title: Comparative genomics of Listeria species.
A;Therence number: AB1077; MUID:21537279; PMID:11679669
                                   glucose 1-dehydrogenase homolog lmo1688 [imported] - Listeria monocytogen C;Specias: Listeria monocytogenes C;Date: 27-Nov-2001 #sequence_revision 27-Nov-2001 #text_change 14-Dec-20 C;Accession: AH1285 R;Glaser, P.; Frangeul, L.; Buchrieser, C.; Amend, A.; Baquero, F.; Berch P; Dominguez-Bernal, G.; Duchaud, E.; Durand, L.; Dussurget, O.; Entian,
.; Dominguez-Bernal, G.; I
D.; Jones, L.M.; Karst, U.
Science 294, 849-852, 2001
                                                                                                                                                              RESULT
AH1285
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AC1657
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A;Experimental source: strain Clip11262
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-248 <GLA>
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
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Best Local Similarity
Matches 77; Conserv
                                                                                                                                                                                                                                              172
                                                                                                                                                                                                                                                                                     183
                                                                                                                                                                                                                                                                                                                             112
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                                                                                                                                                                                                                                                                                                                                                LRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFN-VPYGVGKAACDKLAADCAHELR 182
                                                                                                                                                                                                                                                                                                                                                                                                    NVGDVEKVRALFKAVD-EEFGRLDVFINNAASGVL-----RPIMELEESHWDWIMNIN 111
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLK 217
                                                                                                                                                                                                                                                                                                                                                                                                                               KCV-----VALATDPNILS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NIRGYYFMSIEGGKLMKEHGGGSIINVASINGVSPGEFQGI----YSVTKAAVISMTKVF 175
                                                                                                                                                                                                                                              PFGIAVNAVSGGLIETEALNHFPNREELLKDAVSK
                                                                                                                                                                                                                                                                                                                           AKALLFAGQEAAKLMQRQKSGKIISLSSIGSIRYLENYTTVGVSKAAVESLTRYLAVELA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AVLYLASEASSYTTGVALNVDGGFLS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AHELRRHGVSCVSLWPG1VQTE----LLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GLRGHYFCSVYGARLMVPAGQGLIVVIS----SPGSLQYMFNVPYGVGKAACDKLAADC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IGEMEQIQNVFAQI-REQFGRLDILVNNAATNPQFCNVLETDLGAFQKTV-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17.7%; Score 286.5; DB 35.8%; Pred. No. 6.6e-16;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     36;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           255
                                                                                                                                                                                                                                              206
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 2;
                                                                                                                                         Listeria monocytogenes
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length
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11;

Gaps

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123

171

Maitournam, A. Voss, H.; Wehl

C11p11

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F.; Berche,

14-Dec-200:

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A;Experimental source: strain H37Kv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
A; Residues: 1-255 <C
                                                                                                                                                                                                                                                                                        Query Match
Best Local Similarity
Matches 71; Conserv
                                                                                                                                                                                                                                                                                                                                                                   ;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
;12-194/Domain: short-chain alcohol dehydrogenase homology <SADH>
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Nature 393, 537-544,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C:Species: Mycobacterium tuberculosis
C:Date: 17-Jul-1998 #Sequence_revision 17-Jul-1998 #text_change 20-Jun-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ;Authors: Sqares, R.; Sulston, J.E.; Taylor, K.; Whitehead, S.; Barrell, B.G.;Teference number: A70500; MUID:98295987
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Status; preliminary; nucleic acid sequence not shown; translation not shown
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69 VSQHQQVTSMLDQVTAE-LGGIDIAVCN--AGIITV----TPMLDMPLEBFQRLQNTNV
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                                                   65 SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL 124
                                                                                                                                                172 PFGIAVNAVSGGLIETDALNHFPNREELLKDAVSK 206
                                                                                                            HGKRALITGASTGIGKRVÁLATVEAGAQVAIAARHLDALEKLÁDEIGTSGGKVVPVCCD 68
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                                                                                                                                                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                        16.7%; Score 271; DB 2; Length 25: 34.6%; Pred. No. 1.3e-14; tive 37; Mismatches 83; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17.5%; Score 284.5; DB 2; Length 248; 35.3%; Pred. No. 9.6e-16;
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Voss, H.; Wehland,
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
F;5-185/Domain: short-chain alcohol dehydrogenase homology <SADH>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Cross-references: GB:Z99108; GB:AL009126; NID:g2633055; PIDN:CAB12693.1; PID:g263
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Best Local Similarity
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; A;Aihort H.; Holsabbel, S.; Hosono, S.; Hullo
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R;Kunst, F; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, V.; Carter, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.; Carter, February C.; February
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C:Species: Bacillus subtilis
C:Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text
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                                                                                            120 CAQEAAKLMEKNGGGHÍVSÍSSLGSIRYLENYTTVGVSKAALEALTRYLAVELSEKOIIV 179
180 NAVSGGAIDTDALKHFPNREDLLED 204
                                                                  189 VSLWPGIVQTELLKEHMAKEEVLQD 213
                                                                                                                                                               130 CSVYGARLMVPAGQGLIVVISSPGSLQYMFN-VPYGVGKAACDKLAADCAHELRRHGVSC
                                                                                                                                                                                                                                                                                  70 EVRTLFEQVDREQOGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGHYF 129
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                                                                                                                                                                                                                                                                                                                                                                                       8 LVTGSSRGVGKAAAIRLAENGYNIVINYARSKKAALETÄEEIEKLGVKVLVVKANVGQPA
                                                                                                                                                                                                                                  KIKEMFQQID-ETFGRLDVFVNNAASGVL------RPVMELEETHWDWTMNINAKALLF 119
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33.7%; Pred. No. 6.6e-14;
tive 40; Mismatches 86
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C;Species: Bacillus subtilis
C;Date: 05-Dec-1997 #sequence_revision 05-Dec-1997 #text_change 21-Jul-2000
C;Accession: A69621; PC4176; T46633
R;Kunst, F:; Ogasawara, N.; Moszer, I.; Albertini, A.M.; Alloni, G.; Azevedo, C.; Bron, S.; Brouillet, S.; Bruschi, C.V.; Caldwell, B.; Capuano, V.: Carton
                                                                                                                           3-oxoacyl-[acyl-carrier-protein] reductase (EC 1.1.1.100) [validated] - Bacillus subt
                   V.; Ber
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A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler lech, J.; Harwood, C.R.; Henaut, A.; Hilbert, H.; Holaappel, S.; Hosono, S.; Hullo, M.F. Koetter, P.; Koningstein, G.; Krogh, S.; Kumano, M.; Kurita, K.; Lapidus, A.; Lardinols, A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Levine, A.; Liu, H.; Masuda, S.; Maueel, Y. M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle Rieger, M.; Rivolta, C.; Rocha, E.; Roche, B.; Rose, M.; Sadaie, Y.; Sato, T.; Scanlon, A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Seror akeuchi, M.; Tamakoshi, A.; Tanaka, T.; Terpstra, P.; Tognoni, A.; Tosato, V.; Uchiyama, T.; Winters, P.; Wipat, A.; Yamamoto, H.; Yamane, K.; Yasumoto, K.; Yata, K.; Yoshida, K.; A;Authors: Yoshikawa, H.F.; Zumstein, E.; Yoshikawa, H.; Danchin, A.; A;Tille: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis. A;Accession: A69501
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A; Molecule type: COUP
A; Residues: 230-246 COGUP
A; Cross-references: DDBJ:D64116; NID:g1389548; PIDN:BAA10974.1; PID:g1237012
R; Cronan, J.E.; Morbidoni, H.R.; de Mendoza, D.
Bacteriol. 178, 4794-4800, 1996
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A;Reference number: Z23107; MUID:96326321
A;Accession: T46633
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A;Title: The effect of Srb,
A;Reference number: JC4819;
A;Accession: PC4176
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A;Experimental source: strain 168
R;Gyquro, A.; Kakeshita, H.; Takamatsu, H.; Nakamura, K.; Yamane, K.
Gene 172, 17-24, 1996
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A;Residues: 1-22,'A',24-246 <CRO>
A;Cross-references: EMBL:U59433; NID:g1502418; PIDN:AAC44307.1; PID:g1502421
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A; Residues: 1-246 <KUN>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, sre 390, 249-256, 1997
                                                                                    167
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                                                                                                                                                                                                                                                                                                                                                              61
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              VVALATDPNILSLSGKVL
                                                                                                                                                                                                                  NLKGVFNCTKAVTROMMKORSGRIINVSSIVGVSGNPGQANYV-----AAKAGVIGLTK
                                                                                                                                                                                                                                                                                 GLRGHYFCSVYGARLMVPAGQGLIVVISS-----PGSLQYMFNVPYGVGKAACDKLAA 175
                                                                                                                                                                                                                                                                                                                                                    ADVSNPEDVQNMIKET-LSVFSTIDILVNN--AGI----TRDNLIMRMKEDEWDDVINI
                                                                                                                                                                                                                                                                                                                                                                                                                   CDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MNGQVCVVTGASRGIGRGIALQLCKAGATVYI--TGRHLDTLRVVAQEAQSLGGQCVPVV 62
                                                                             SSAKELASRNITVNAIAPGFISTD-MTDKLAKD--VQDEMLKQIPLA-RFGEPSDVSS--
                                                                                                                                               DCAHELRRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LNDKTAIVTGASRGIGRSIALDLAKSGANVVVNYSGNEAKANEVV-DEIKSMGRKAIAVK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           77; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 15.7%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  46; Mismatches 105;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Score 254; DB:
Pred. No. 2.9e-
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glucose 1-dehydrogenase BH0938 [imported] - Bacillus halodurans (strain C-1: C;Species: Bacillus halodurans C;Species: Bacillus halodurans C;Species: Dec-2000 #sequence_revision 01-Dec-2000 #text_change 15-Jun-2001 C;Accession: B83767 C;R;Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; FNucleic Acids Res. 28, 4317-4331, 2000
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A;Residues: 1-249 <STO>
A;Cross-references: GB:AP001510; GB:BA000004; NID:g10173440;
A;Experimental source: strain C-125
C;Genetics:
A;Gene: BH0938
                  C;Species: Eubacterium sp.
C;Date: 10-Sep-1999 *sequence_revision 10-Sep-1999
C;Accession: A42468; A36439
R;Baron, S.F.; Franklund, C.V.; Hylemon, P.B.
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J. Bacteriol. 173, 4558-4569, 1991
                                                                                                                  7alpha-hydroxysteroid dehydrogenase (EC 1.1.1.159) -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local S
Matches 76
                                                                                                                                                                                                                                                                             242
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                                                                                                                                                                                                                                                                           DPNIL 246
                                                                                                                                                                                                                                                                                                                          APKNIVVNAVSGGAVDTDALTHFPNRDELLEDAAKR--TPAGKIVEPSDLANAVLFLLSE
                                                                                                                                                                                                                                                                                                                                                                                                                AL---LFCAQEAAKRMEKNGGGKIVSLSSLGAIRYLKNYTTVGVSKAAVEALTRYLAVEL
                                                                                                                                                                                                                                                                                                                                                                                                                                                     GLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFN-VPYGVGKAACDKLAADCAHEL 181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NVGKRDKIEELFAQID-DTYGRLDVFVNNAASGVLRPLMELEESHWD-----WTMDINSK 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWD-DINNV 122
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MERKVALVTGSSRGIGKEIALRLADRGYDLVINYARSRKAAEETAAEIEQKGVKALIVKA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MNGQVCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCVPVVC
                                                                                                                                                                                                                                                                                                                                                                 RRHGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALAT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                h 15.2%; Score 247; DB 2; Length 249; Similarity 31.0%; Pred. No. 1.1e-12; 76; Conservative 46; Mismatches 109; Indels
                                                                        #text_change 10-Sep-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PIDN:BAB04657.1; GSPDB:
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                                                                                                                  (strain VPI 127
                                                                                                                                                                                                                                                                                                                                                                   241
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                                                                                                                                                                                                                                                                                                                                                                                                                171
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A;Cross-references: GB:M58743
A;Note: the authors translated the codon CCC for residue 95 as Phe, and CCG for res R;Franklund, C.V.; de Prada, P.; Hylemon, P.B.
J. Biol: Chem. 265, 9842-9849, 1990
A;Title: Purification and characterization of a microbial, NADP-dependent bile acid A;Reference number: A36439; MUID:90277676
A;Accession: A36439
A;Status: preliminary

A; Molecule type: protein A; Residues: 1-22 <FRA> C; Superfamily: ribitol do

ribitol dehydrogenase; short-chain alcohol dehydrogenase homology

A;Reference number: A42468; MUID:91310560 A;Accession: A42468

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coding

for bile acid 7alpha

A;Status: preliminary A;Molecule type: DNA A;Residues: 1-266 <BAR>

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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase, homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA Res. 8, 205-213, 2001
A;Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana
A:Reference number: AB1807; MUID:21595285; PMID:11759840
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguch
Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Yasuda, M.; Tabata,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A:Note: Anabaena sp. (strain PCC 7120) is a synonym of Nostoc sp. strain PCC 7120 C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 11-Jan-2002
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: GB:BA000019; PIDN:BAB73593.1; PID:g17130984; GSPDB:GN00179
A;Exper1mental source: strain PCC 7120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-251 < KUR>
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                                                                                                                                                                                                                                                                                                                                      Query Match 13.4
Best Local Similarity 31.0
Matches 85; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        3-oxoacyl-[acyl-carrier protein] reductase [imported] - Anabaena sp. (strain PCC 7120)
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F;6-188/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ouery Match
Best Local Sim
Matches 78;
                                                            176 DCAHELRRHGVSGVSLWPGIVOTELLKEHWAKEEVLQDPVLKQFKSAFSSAETTELSGKC 235
                           173 TVAKELASRGITVNAVAPGFIATD-MTSNLKSEGILQYIPLGRY------GOPEETAG-M 224
                                                                                                    113 QAVIDLNLTGVFLCTRAVSKLMLKORSGRIINITSVAGOMGNPGQANYSAAKAGVIGFTK 172
                                                                                                                                       117 DDINNVGLRGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAA 175
                                                                                                                                                                             67 ADVSQ------YEQVDNLINGAIDKFKRIDILVNN--AGI----TRDTLLLRMKPEDW
                                                                                                                                                                                                              63 CDSSQESEVRTLFEQVDREQOG------RLDVLVNNAYAGVQTILNTRNKAFWETPASMW 116
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       224 AAVVYFASDDAAYTTGQILTVSG 246
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             234 KCVVALATDP-----NILSLSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  174 HEARHNIRCNAVLPGMTAT------DAVQDNLTDDFRNFFLKHTPIQRMGLPEEIA 223
                                                                                                                                                                                                                                                                                         5 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTL--RVVAQEAQSLGGQCVPVV 62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        180 ELRRHGVSCVSLWPGIVOTELLKEHMAKEEVLODPVLKQFKSAFSSAETTELSG-----
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  121 NVGLRGHYFCSVYGARLMVPAGOGLIVVISSPGSL-QYMFNVPYGVGKAACDKLAADCAH 179
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               63
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VVALATOPNILSLSGKVLPSCDLARRYGLRDVDG
                                                                                                                                                                                                                                                     LRGQVAVVTGASRGIGRAIALELANYGATVVVNYASSSTAADEVVA-EITGAGGEAVALK 66
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NINLKSVFIASQTAVKYMAENGGGSIINISSVGGLIPDISQIAYGTSKAAINYLTKLIAV 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SSQESEVRTLFEQVDREQOGRLDVLVNNAYAGVQT----ILNTRNKAFWETPASMWDDIN 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATKEETYVTMIEEI-IEQEGRIDVLVNNFGSSNPKKDLGIANTDPEVFIKTV----- 113
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LKDKVILVTASTRGIGLAIAQACAKEGAKVYMGARNLERAKARADEMNAAGGNVKYYYND
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                                                                                                                                                                                                                                                                                                                                Score 246; DB 2; Length 25
Pred. No. 1.3e-12;
39; Mismatches 106; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               250
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                                                                                                                                                                                                                                                                                                                                                                         Length 251;
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                                                                                                                                                                                                                                                                                                                                    44;
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                                                                                                                                                                                                                                                                                                                              Gaps
                                                                                                                                                                             112
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Best Local Similarity
""+"ches 87; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                         C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Cross-references: GB:AE004831; GB:AE004091; NID:g9950347; PIDN:AAG07535.1; GSPDB:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA A; Residues: 1-266 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Reference number: A82950; MUID:20437337.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Accession: F83127
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, P.; Hickey, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas, A.; Larbig,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               probable short-chain dehydrogenase PA4148 [imported] - Pseudomonas aeruginosa
C;Species: Pseudomonas aeruginosa
C;Date: 15-Sep-2000 #sequence_revision 15-Sep-2000 #text_change 31-Dec-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .; Lory, S.; Olson, M.V. Nature 406, 959-964, 2000
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231 Q-----GEAQTVEDMGQLVVYLACAPHV
                             218 OFKSAFSSAETTELSGKCVVALATDPNI 245
                                                      171 GFSNALAKEVARDGVTVNALCPGIVGTGMWRGEDGLSGRWRQAGESEAQSWERHQASLLP 230
                                                                                                              178
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                                                                                                                                                                              125
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                                                                                                                                                                                                                  65 SSQESEVRTLFEQVDREQOGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL
                                                                                                                                                                                                                                                           11 LSSRVALVTGAGRGIGRGIALALARAGADVAVADLDPQVAEETAAAIRSLGRRSLALGVD 70
                                                                                                                                                                                                                                                                                225 VRFLAADPAAAYITGQVF---
                                                                                                -----AHELRRHGVSCVSLWPGIVQTELLK-----
                                                                                                                                  RGVFLCCQAELPLMQAQRWGRIVNLSSI-----
                                                                                                                                                          RGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNVPYGVGKAACDKLAADC-----
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                                                                                                                                                                                                                                                                                                                                                    15.0%;
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                                                                                                                                                                                                                                                                                                                                                   Score 243; DB 2;
Pred. No. 2.5e-12;
                                                                                                                                                                                                                                                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ---NVDG 246
                                                                                                                           ---AGKVGLPDLAHYCASKFAVI
                                                                                         ----EHMAKE-EVLQDPVLK 217
                                                                                                                                                                                                                                                                                                                                                                 Length 266
                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                          Gaps
                                                                                                                                                              177
                                                                                                                                                                                                                             124
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OM protein -
protein search, using sw model
                                                                     GenCore version 4.5 Copyright (c) 1993 - 2000 Compugen Ltd.
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July 31, 2002, 15:09:21; Search time 13.44 Seconds (without alignments) 901.728 Million cell updates/sec

Run on:

Title: Perfect score: Sequence: US-10-006-163-1 1623 1 MAAPMNGQVCVVTGASRGIG.....YLPSFLRVPKWIIALYTSKF 313

Scoring table:

Searched:

BLOSUM62 Gapop 10.0 , Gapext 0.5

105224 seqs, 38719550 residues

Total number of hits satisfying chosen parameters: 105224.

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

Database :

SwissProt\_40:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution. Pred. No.

#### SUMMARIES

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| Result<br>No. S | 5 i B | Query<br>Match Le |                  | DB<br>1    | ID .        |    | Description | bacillus su  |
|-----------------|-------|-------------------|------------------|------------|-------------|----|-------------|--------------|
| N               | S     |                   | 271              | ٠,         | SDR1_PICAB  | ÷  | N           | picea abies  |
| J               | 222   | 13.9              | 260              | ــر د      | TRN2_DATST  |    |             | datura s     |
| UT A            | 22:   |                   | 248              | <b>-</b> + | FABG AOUAE  |    | 067610      | agulfex ae   |
|                 |       |                   | 256              | ۳          | GNO_GLUOX   |    | P50199      | qluconobac   |
|                 | 217.5 | •                 | 246              | ب          | FABG_THEMA  | •  | Q9x248      | thermotoga   |
| 80              | 215   |                   | 247              | -          | FAG1_SYNY3  |    | P73574      | synechocys   |
| 9               | 214   | •                 | 260              | ۳          | TRN2_HYONI  |    | P50164      | hyoscyamus   |
| 10              | 214   | •                 | 320              | _          | FABG_CUPLA  |    |             | cuphea la    |
| 11 2            | 13.5  | •                 | 275              | μ          | YCP1_BRAJA  |    |             | bradyrhizol  |
| 12              | 209   | •                 | 256              | _          | Y019_THEMA  |    | Q56318      | thermotoga   |
| 13              | 206   | •                 | 319              | Н          | FABG_ARATH  | :  | P33207      | arabidops    |
|                 | 204   | 12                | 262              | -          | YXBG_BACSU  |    | P46331      | bacillus     |
|                 | 03.5  | 5.5               | 255              | -          | HDHA_ECOLI  |    | P25529      | escherichia  |
|                 | 200   | 5                 | 238              | _          | YOXD_BACSU  |    | P14802      | bacillus     |
|                 | 193   | Ε                 | 313              | ۲          | YXEK_CAEEL  |    | Q93761      | caenorhabd   |
|                 | 192   | : =               | 592              | ۔ ،        | EPHD_MYCTU  |    | Q10402      | mycobacter   |
|                 | 1 2   | : =               | 102              | ٠          | Y325_THEMA  |    | OBAMAGO     | thermotog    |
|                 | 100   | 11.7              | 261              | ۳,         | ACT3_STRCO  | ,  | P16544      | streptomyce  |
|                 | 20 10 | 11.7              | )<br>N<br>N<br>N | - ۱        | HUHA_CLOSO  | •  | P50200      | clostric     |
|                 | 8     | 11.6              | 247              | ۱ د        | EABU DOEAE  |    | 0740400     | A FOR STORES |
|                 | 186   | =                 | 336              | <b>-</b> 1 | ξ.          | :, | P50160      | zea mavs     |
|                 | .85.5 | 11.4              | 253              | -          | KDUD_ECOLI. | :: | P37769      | escherichia  |
|                 | 85.5  | 11.4              | 263              | <b>-</b>   | UCPA_SALTY  |    | P37441      | salmonella   |
|                 | 185   | 11.4              | 244              | _          | FABG_VIBHA  | •  | P55336      | vibrio ha    |
|                 | 185   | 11.4              | 258              | -          | BDHA_RHIME  | ٠. | 086034      | rhizobium m  |
|                 | 185   | 11.4              | 272              | -          | DHK1_STRVN  |    | P16542      | streptomyc   |
|                 | .84.5 | 11.4              | 253              | <b>-</b>   | KDUD_ERWCH  |    | Q05528      | erwinia chr  |
|                 | 83.5  | 11.3              | 242              | -          | FABG_ACTAC  |    | P70720      | actinobac    |
|                 | 83.5  | _                 | 248              | -          | Y4EK RHISN  |    | P55434      | rhizobium    |
|                 | ,     | ,                 | ,                | ۲          | i           |    |             |              |

| 34 182.5 11.2 263 1 UCPA_ECOLI 35 181 11.2 247 1 VD50_MYCTU 36 181 11.2 261 1 BEND_ACICA 37 180.5 11.1 254 1 IDNO_ECOLI 38 179.5 11.1 254 1 IDNO_ECOLI 40 176 10.8 241 1 BABG_HAEIN 41 176 10.8 244 1 FABG_VIECH 42 176 10.8 244 1 FABG_VIECH 43 175.5 10.8 254 1 DHG_BACME 44 175 10.8 254 1 DHG_BACME 45 173.5 10.7 262 1 DHGB_BACME 47 175 10.8 244 1 FABG_ECOLI 48 175 10.8 254 1 DHGB_BACME 49 175 10.8 260 1 DHGB_BACME 40 176 10.8 270 1 PAGB_BCOLI 41 175 10.8 270 1 PAGB_BCOLI 42 176 10.8 270 1 PAGB_BCOLI 43 175.5 10.8 270 1 PAGB_BCOLI 44 175 10.8 270 1 PAGB_BCOLI 45 173.5 10.7 262 1 DHGB_BACME 46 177 170 170 170 170 170 170 170 170 170    |            |            |           |                 |            |            |            |            |            |            |            |               |
|---|------------|------------|-----------|-----------------|------------|------------|------------|------------|------------|------------|------------|---------------|
| 11.2 263 1 UCPA_ECOLI 11.2 247 1 YD50_MYCTU 11.2 247 1 BEND_ACICA 11.2 241 1 BEND_ACICA 11.1 254 1 IDNO_ECOLI 11.1 254 1 IDNO_ECOLI 11.1 242 1 FABG_HAEIN 11.1 242 1 FABG_WOUSE 10.8 241 1 BUDC_KLETE 10.8 241 1 FABG_VIECH 10.8 244 1 FABG_VIECH 10.8 254 1 KUUD_BACSU 10.8 254 1 FABG_ECOLI 10.8 255 1 DHGB_BACME 10.8 262 1 DHGB_BACME 10.8 263 1 DHGB_BACME 10.8 264 1 FABG_ECOLI | 45         | 44         | 43        | 42              | 4          | 40         | 39         | 38         | 37         | 36         | 35         | ω<br><b>4</b> |
| 263 1 UCPA_ECOLI 247 1 YD50_WYCTU 247 1 D50_WYCTU 241 1 END_ACICA 254 1 IDNO_ECOLI 242 1 FABG_HAEIN 260 1 DHBB_MOUSE 241 1 FABG_VIECH 244 1 FABG_VIECH 254 1 KDUD_BACSU 254 1 KDUD_BACSU 254 1 FABG_BCOLI 254 1 FABG_BCOLI 254 1 FABG_BCOLI 255 1 DHGB_BACME 255 1 DHGB_BACME 256 1 DHGB_BACME 257 16 DHGB_BACME 258 1 PABG_BCOLI 259 1 DHGB_BACME 269 1 DHGB_BACME 279 1 DHGB_BACME   | 173.5      | 175        | 175.5     | 176.            | 176        | 176        | 179        | 179.5      | 180.5      | 181        | 181        | 182.5         |
| 1 UCPA_ECOLI  | 10.7       | 10.8       | 10.8      | 10.8            | 10.8       | 10.8       | 11.0       | 11.1       | 11.1       | 11.2       | 11.2       | 11.2          |
| P37440<br>Q11020<br>P07777<br>P07777<br>P39345<br>P50171<br>Q4450<br>Q9kqh7<br>P50842<br>P40228<br>P25716   | 262        | 244        | 261       | 254             | 244        | 241        | 260        | 242        | 254        | 261        | 247        | 263           |
| P37440<br>Q11020<br>P07772<br>P07773<br>P39345<br>P50171<br>Q04520<br>Q9kqh7<br>P50842<br>P40228<br>P25716<br>P07999  | _          | <u> </u>   |           | ᆫ               | ۱          | <b>-</b>   | _          | _          | ب          | _          | μ          | H             |
| P37440 escherichia Q111020 mycobacteri P07772 a c1s-1,2-d P39345 escherichia P43713 haemophilus P50371 mus musculu Q04520 klebsiella Q9kqh7 vibrio chol P50842 bacillus me P40788 bacillus me P25716 escherichia  | DHGB_BACME | FABG_ECOLI | DHG_BACME | KDUD_BACSU      | FABG_VIBCH | BUDC_KLETE | DHB8_MOUSE | FABG_HAEIN | IDNO_ECOLI | BEND_ACICA | YD50_MYCTU | UCPA_ECOLI    |
| 40 escherichia 20 mycobacteri 2 a cis-1,2-d 45 escherichia 13 haemophilus 13 haemophilus 14 haemophilus 15 haemophilus 16 escherichia 17 vibrio chol 18 bacillus me 18 escherichia 19 bacillus me   | P079       | P257:      | P4021     | P508            | Q9kq1      | 2045       | P501       | P437:      | . P393     | P077       | Q110;      | · P374        |
| escherichia mycobacteri a cis-1,2-d escherichia haemophilus hus musculu klus musculu klus illa vibrio chol bacillus su bacillus me escherichia bacillus me  | 99         | 9          | 88        | 2               | 7          | 20         | 71 -       | <u></u>    | 5          | 72         | 8          |               |
|   | baci       | escher     | pacillu:  | <b>pacillus</b> | vibrio c   | klebsiel:  | nus muscı  | haemophi:  | escherich  | 1 cis-1,   | nycobact   | escheric      |

## ALIGNMENTS

|  | 9            |    |
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| (SDR) FAMIL  |              |    |
| SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES     | <u>.,</u>    | _  |
| PATHWAY.   |              | _  |
| PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS         | <del>:</del> | _  |
| NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.                  |              | _  |
| (3R) - 3 - hydroxyacyl - [ac;  | -            | _  |
|  | Subn         | _  |
|  |              | _  |
|  | RC STRAIN    | _  |
| SEQUENCE OF 230-246 FROM N.A.  |              | _  |
| •  |              |    |
| Microbiology 144:801-805(1998).                                      |              | _  |
|  |              | _  |
| "A 28 kbp segment from the spoVM region of the Bacillus subtilis 168 |              | _  |
| ger D., Errington J.;  |              |    |
| MEDLINE=98195738; PubMed=9534248;                                    |              | _  |
|  |              | _  |
| SEQUENCE OF 1-172 FROM N.A.:   | RP SECUEN    |    |
|  |              |    |
| Ogasawara N., Yoshikawa H., Danchin                                  |              |    |
| 8;   |              | -  |
| ENCE FROM N.A.   |              | -  |
|  | [2]          | -  |
|  |              | -  |
| synthesis genes.";   |              | -  |
| subtilis acyl carrier protein is                                     |              |    |
| H.R., de Mendoza D., Cronan J.                                       |              | -  |
| MEDLINE-96326321; PubMed-8759840;                                    |              | -  |
| σ  |              |    |
| ENCE FROM N.A.   | RP SECTIENCE |    |
| [1]  |              |    |
| NCRI TANTOLADA:  | TATANG YOU   | ٠, |
| •  |              |    |
|  |              |    |
|  |              |    |
| acyl carrier protein reductase).                                     |              |    |
| oacyl-[acyl-carrier_protein] reductase (EC 1.1.1.100) (3-ketoacyl-   |              | _  |
| te)  |              | _  |
| EC-1998 (Rel. 37, Last sequence update)                              | DT 15-DEC    | _  |
| CT-1996 (Rel. 34, Created)   |              | _  |
| •  |              | -  |
| _BACSU STANDARD; PRT; 246 AA.  | ID FABG_E    |    |
| <b>a</b>   | FABG_BACSU   |    |
|  | RESILT 1     |    |
|  |              |    |

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EMBL; 299112; CAB13464.1; EMBL; Y13937; CAA74250.1; EMBL; D644116; BAA10974.1; HSSP; P50162; 1AE1. Subtilist; BG11535; fabG.

CAB13464.1; CAA74250.1; BAA10974.1;

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Q1-OCT-1996
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
01-OCT-1996 (Rel. 34, Last sequence update)
Short-chain type dehydrogenase/reductase (EC 1...-).
Picea abies (Norway spruce) (Picea excelsa).
Ewkaryota; Viridiplantae; Streptophyta; Embryophyta; Ti
Spermatophyta; Coniferopsida; Coniferales; Pinaceae; Pi
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A. MEDLINE-94120027;
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ACT_SITE
CONFLICT
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                                                                                                                                                                                                                                                                                                                                                                               Isolation and characterization of a cDNA clone hort-chain alcohol dehydrogenase from Norway. sp
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       221
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                236
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                                                                                                                                                                                                                                                                                or Physic1. 103:1479-1480(1993).
SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                      (SDR) FAMILY.
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D.;
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77; Conser
                            email to
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23
246 AA;
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23
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D -> A (IN REF. 1).
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Pred. No. 6.7e-14;
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Picea.
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Best Local
                                                                                                                           Makajama ... - ... Yamada Y .;
Hashimoto T. Oda J., Yamada Y .;
"Crystal structures of two tropinone reductases:
stereospecificities in the same protein fold.";
stereospecificities in the same protein fold.";
stereospecificities in the same protein fold.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-0CT-1996
01-0CT-1996
16-0CT-2001
Yamashita A., Kato H., Wakatsuki S., Tomizaki T.,
Nakajima K., Hashimoto T., Yamada Y., Oda J.;
"Structure of tropinone reductase-II complexed win
                                                                                                                                                                                                                  X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS).
MEDLINE-98226735; PubMed-9560196;
Nakajima K., Yamashita A., Akama H., Nal
Hashimoto T., Oda J., Yamada Y.;
                                                                                                                                                                                                                                                                                                                                   Nakajima K., Hashimoto T., Yamada Y.;
"Two tropinone reductases with different stereospecificities short-chain dehydrogenases evolved from a common ancestor.";
Proc. Natl. Acad. Sci. U.S.A. 90:9591-9595(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TRN2_DATST P50163;
                                                                        X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-99316165; PubMed-10387002;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Datura stramonium (Jimsonweed) (Common thornapple).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheo Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Asteridae; euasterids I; Solanales; Solanaceae; Datura.
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ACT_SITE
SEQUENCE
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HSSP; Q12634; 1YBV.
InterPro; IPR002198; ADH_short.
pfam; pF00106; adh_short; 1.
pRINTS; PR00080; SDRFAMILY.
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001 (Rel. 40, Last anno
e reductase-II (EC 1.1.
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RESULT 4
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ID Y4LA_RHISN
AC P55541;
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Best Local Similarity 28.7
Matches 70; Conservative
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01-NOV-1997
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ACT_SITE
                                            Rhizobium sp. (strain NGR234).
Plasmid sym pNGR234a.
Bacteria; Proteobacteria; alph
SEQUENCE FROM N.A
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Ox1doreductase; NADP; 3D-structure.
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                      NCBI_TaxID=394;
                                     Rhizobiaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 InterPro; IPR002198; ADH_short.
Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRPAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              pean Bioinformatics Institute. There are no restrictions on its non-profit institutions as long as its content is in no way and this statement is not removed. Usage by and for commercial requires a license agreement (See http://www.isb-sib.ch/announce/
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(Rel. 35,
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                                     Rh1zobium
                                                                                                                                                                STANDARD;
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28311 MW;
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Pred. No. 1.5e-11;
9; Mismatches 113
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BY SIMILARITY.
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067610;
15-DEC-1998
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ACT_SITE
SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Perret X.; "Molecular basis of symbiosis between Nature 387:394-401(1997).
  Nature
                              Deckert G., Warren P.V., Gaasterland T., Young W. Graham D.E., Overbeek R., Snead M.A., Keller M., Feldman R.A., Short J.M., Olson G.J., Swanson R.V. "The complete genome of the hyperthermophilic bac
                                                                                                                      Aquifex aeolicus.
Bacteria; Aquificales;
NCBI_TaxID=63363;
                                                                                                                                                     acyl carrier pro
FABG OR AO_1716.
                                                                                                                                                                          15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase (E
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                                                                          MEDLINE-98196666; PubMed-9537320;
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 CATALYTIC ACTIVITY:
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278 AA;
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Huber
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Best Local S
Matches 72
                                                                                                                                                                                                                                                                                    GNO_GLUOX
P50199;
01-OCT-1996
        Klasen R., Bringer-Meyer S., Sahm H.;

**Blochemical characterization and sequence analysis of the gluconate: NADP 5-oxidoreductase gene from Gluconobacter ox J. Bacteriol. 177:2637-2643(1995).

-I- FUNCTION: INVOLVED IN THE NONPHOSPHORYLATIVE, KETOGENI OF GLUCOSE AND OXIDIZES GLUCONATE TO 5-KETOGLUCONATE. NADP, ALMOST INACTIVE WITH NAD.
                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
Gluconate 5-dehydrogenase (EC 1.1.1.69) (5-keto-b-gluconate
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NP_BIND
ACT_SITE
SEQUENCE
                                                                                                          SEQUENCE FROM N.A., SEQUENCE OF 3 STRAIN-DSM 3503; MEDLINE-95270578; PubMed-7751271;
                                                                                                                                                                                         Bacteria; Proteobacteria;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                 NCBI_TaxID=442;
                                                                                                                                                                                                                                     reductase).
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PATHWAY:
SIMILARITY: BELA
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ND 12 36 NADP (BY SIMILARITY)
ITE 157 157 BY SIMILARITY
NCE 248 AA; 26867 MW; SCFD9EB9AD83F2C5 CRC64;
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34,
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                                                                                                                                     SEQUENCE OF 3-19,
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cla; alpha subdivision; Acet
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D-gluconate + NAD(P)(+) = 5-dehydro-D
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Best Local S
Matches 66
                     SEQUENCE FROM N.A.

STRAIN-MSB8 / DSM 3109;

MEDLINE-9287316; PubMed-10360571;

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Nelson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.S.,

McDonald L., Utterback T.R., Malek J.A., Hinher K.D., Garrett M.D.,

McDonald L., Utterback T.R., Malek J.A., Hinher K.D., Garrett M.D.,

McDonald L., Utterback T.R., Malek J.A., Hinher K.D., Garrett M.D.,

McDonald L., Utterback T.R., Malek J.A., Hinher K.D., Garrett M.D.,

McDonald L., Utterback T.R., Malek J.A., White O.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.,

"Eyidence for lateral gene transfer between Archaea and Bacteria fr
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SEQUENCE
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PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT;
                                                                                                                                                                                                                                                                                                                                                         Thermotoga maritima.
Bacteria; Thermotogales;
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30-MAY-2000 (Rel. 39, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation updat
3-oxoacyl-(acyl-carrier protein) reductase
acyl carrier protein reductase).
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SUBUNIT: HOMODIMER.
SUBCELLULAR LOCATION:
SIMILARITY: BELONGS TO
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                   of Thermotoga maritima.";
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Best Local :
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P73574;
15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
16-OCT-201-[acyl-carrier protein] reductase 1 (EC 1.1.1.100)
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MEDLINE=97061201; PubMed=8905231;

Kaneko T., Sato S., Kotani H., Tanaka A., Asamizu
Miyajima N., Hirosawa M., Sugiura M., Sasamoto S.
Hosouchi T., Matsuno A., Muraki A., Nakazaki N.,
Shimpo S., Takeuchi C., Wada T., Watanabe A., Yam
Tabata S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SYNY3
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HSSP; P50162; 1AE1.
TIGR; TM1724; -.
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                                                                                                                                                                                                                                                                                                                      Synechocystis sp. (strain Bacteria; (yanobacteria; )
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FABG1 OR SLR0886.
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PF00106; adh_short; 1.
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P50164;
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01-OCT-1996 (Rel. 34,
16-OCT-2001 (Rel. 40,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Sequence analysis of the genome of the unicellular cyanobacterium Synechocystis sp. strain PCC6803. II. Sequence determination of the entire genome and assignment of potential protein-coding regions."; DNA Res. 3:109-136(1996).

1- CARLYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein] + NADP(+) = 3-0x0acyl-[acyl-carrier protein] + NADPH.

1- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                          Hyoscyamus niger (Henbane).
Eukaryota; Viridiplantae; Str.
Epermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      use by non-profit institutions as long as its content is modified and this statement is not removed. Usage by and foentities requires a license agreement (See http://www.isb-slb.or send an email to license@isb-slb.ch).
                                                   Asteridae;
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TISSUE-Cultured
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                                  Asteridae; euasterids
NCBI_TaxID=4079;
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TTE 156 156 BY SIMILARITY.
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                   FABG_CUPLA STANDARD; PRT; 320 AA P.28643; Ol-DEC-1992..(Rel. 24, Created) Ol-DEC-1992 (Rel. 24, Last sequence update) 16-OCT-2001 (Rel. 40, Last annotation updat.) 3-oxocyl-[acyl-carrier protein] reductase, (EC 1.1.1.100) (3-ketoacyl-acyl carrier pro
Cuphea
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PROSITE; PS00061; ADH_SI
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EMBL; AB026545; BAA85845.1;
HSSP; P50163; 2AE2.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nakajima K., Hashimoto T.;
"Tropinone reductase-II gene of Hyoscyamus niger.";
Submitted (APR-1999) to the EMBL/GenBank/DDBJ databases.
-i- FUNCTION: CATALYZES THE STEREOSPECIFIC REDUCTION OF
                                                                                                                                                                                                                                                                                                              120
                                                                                                                                                                                                                                                                                                                                          125
                                                                                                                                                                                           226 KELA 229
                                                                                                                                                                                                                      244 NILS
                                                                                                                                                                                                                                                                                 184
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDLINE-94120020; PubMed-8290643;
Nakajima K., Hashimoto T., Yamada Y.;
"CDNA encoding tropinone reductase-II
Plant Physiol. 103:1465-1466(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "CDNA encoding Plant Physical.
                                                                                                                                                                                                                                                                                                                                                                       67
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   nterPro;
                                                                                                                                                                                                                                                                                                                                                                                                    65
                                                                                                                                                                                                                                                                                                                                                                                                                                                             5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CATALYTIC ACTIVITY: Pseudotropine + NADP(+) = tropinone + NADPH. PATHWAY: BIOSYNTHETIC PATHWAY OF TROPANE ALKALOIDS. SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                            DNIRVNGVGPGVIATSMV-----EMTIQDPEQKE-----
                                                                                                                                                                                                                                                                                                                                                          LSSRSEREEFMKTVSNHFHGKLNILVNN--AGIVIYKEAKDYTMED-----YSHIMSINF
                                                                                                                                                                                                                                                                                                                                                                                                                                      MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQSLGGQCVPVVCD 64
                                                                                                                                                                                                                                                                   HGVSCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALATDP
                                                                                                                                                                                                                                                                                                  EAAYHLSVLAHPFLKASERGNVVFISSISGASALPYEAVYGATKGAMDQLTRCLAFEWAK
                                                                                                                                                                                                                                                                                                                          RGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCAHELRR 183
                                                                                                                                                                                                                                                                                                                                                                                      SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETFASMWDDINNVGL
                                                                                                                                                                                                                                                                                                                                                                                                                     LEGCTALVTGGSRGIGYGIVEELANLGASVYTCSRNQKELDECLTQWRSKGFNVEASVCD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (SDR) FAMILY.
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lanceolata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          65;
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                                                                                                                                                                                                                     247
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159
260
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Conservative
                  el. 40, Last annotation update)
1-carrier protein] reductase, chloroplast precursor
(3-ketoacyl-acyl carrier protein reductase).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADH_SHORT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            159 B
28437 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   13.2%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       39;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 214; DB 1;
Pred. No. 1.4e-10;
9; Mismatches 118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ۲.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NADP (BY SIMILARITY).
BY SIMILARITY.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         6CA7AF85CAA128FC CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 from
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Hyoscyamus niger.";
                                                                                                                                                                                                                                          -NLDKLIDRCALRRMGEP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 260;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  .Indels
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NP_BIND
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                               "Isolation and characterization of a cDNA from Cuphea lanceolata encoding a beta-ketoacyl-ACP reductase.";

MO1. Gen. (233:12-128(1992).

-i- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]

NADP(+) = 3-oxoacyl-[acyl-carrier protein] + NADPH.

-i- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                           HSSP; P50162; lAE1.
InterPro; IPR002198; ADH_short.
                                                                                                                                                                                           EMBL; X64566; CAA45866.1; -. PIR; S19832; S19832.
                                                                                                     Fatty acid biosynthesis;
                                                                                                                                 PRINTS; PRO0080; SDRFAMILY
                                                                                                                                                  Pfam; PF00106; adh_short;
                                                                                                                                                                                                                                                                                                                                                                     <del>:</del>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Klein B., Pawlowski
Toepfer R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE FROM N.A. MEDLINE-92293104; PubMed-1376402;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota; Viridiplantae; Streptophyta; Embryospermatophyta; Magnollophyta; eudicotyledons; eurosids II; Myrtales; Lythraceae; Cuphea.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NCBI_TaxID=3930
                                                                                       ransit peptide.
                                                                                                                                                                                                                                                                                                                                                                                          SUBURIT: HOMOTETRAMER SUBCELLULAR LOCATION:
                                                                                                                                                                                                                                                                                                                                                               SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                    PLASTIDS
                                                                                                                                                                                                                                                                                                                                                     (SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                             PATHWAY.
                                                                                                                     PS00061;
   82
227
320
                                                               62
    AA;
                                                                                                                     ADH_SHORT;
   106
227
33103
                                                          61
320
                                                                                                                                                                                                                                                                                                                                                         TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoericke-Grandpierre C.,
    MW;
                                                                                                Oxidoreductase; NADP; Chloroplast;
                                                                                                                                                                                                                                                                                                                                                                                            (PROBABLE).
CHLOROPLAST
                ВΥ
                                          CHLOROPLAST (BY SIMILARITY)
3-OXOACYL-[ACYL-CARRIER PRO]
REDUCTASE.
                            NADP (BY SIMILARITY).
06BAF0522B2BBC87 CRC64;
                  SIMILARITY
                                                                                                                                                                                                                                                                                                                                                                                       AND NON-PHOTOSYNTHETIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Embryophyta; Tracheophyta;
edons; core eudicots; Rosid:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Schell
                                                       PROTEIN
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Query Match
Best Local
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                                                                                                                                                                                                                                                      9 VCVVTGASRGIGRGIALQLCKAGATVYIT-GRHLDTLRVVAQEAQSLGGQCVPVVCDSSQ
                SLSGKVLPSCDLARRYGLRDVDGRPVQDYLSLSSVLSHVSG
                                                           NVNAVAPGFISSDMTSK---
                                                                                                            FLCTQAAAKIMMKKKKGRIINIASVVGLVGNAGQANYSAAKAGVIGFTKTVAREYASRNI
                                                                                SCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALATDPNIL
                                                                                                                                     YFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCAHELRRHGV
                                                                                                                                                                   EEDVEAMIKTA-VDAWGTVDILVNN--AGI----TRDGLLMRMKKSQWQEVIDLNLTGV
                                                                                                                                                                                          ESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGH
                                                                                                                                                                                                                         VVIVTGASRGIGKAIALSLGKAGCKVLVNYARSSKEAEEVSKEIEAFGGQALTFGGDVSK
                                                                                                                                                                                                                                                                                                        Similarity
·KILETIPLGRYGQPEEVAG--LVEFLAINPASSYVTG
                                                                                                                                                                                                                                                                                         Conservative
                                                                                                                                                                                                                                                                                                     13.28;
                                                                                                                                                                                                                                                                                        51;
                                                                                                                                                                                                                                                                                   Score 214; DB 1;
Pred. No. 1.8e-10;
1; Mismatches 108
                                                                                                                                                                                                                                                                                      108;
                            287
                                                                                                                                                                                                                                                                                                               Length 320
                                                                                                                                                                                                                                                                                     Indels
                                                                                                                                                                                                                                                                                   52;
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YCP1_BRAJA
AC 0.45219;
DT 01-NOV-1997
DT 01-NOV-1997
DT 15-DEC-1998
DE PRODADLE Sh
OCS BARDYThizob:
OC BARDYTHIZOB
RT SEQUENCE FR
RC STRAIN-USDA
RA TULLY R.E.,
RT "CLONING AN
ACTIVE SEQUENCE FR
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RT BRADYTHIZOB
STRAIN-USDA
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RT "LACHTIFICA
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Best Local S
Matches 65
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15-DEC-1998 (Rel. 37, Last sequence update)
Probable short-chain type dehydrogenase/reductase (EC 1.-.-).
Bradyrhizoblum japonicum.
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Bradyrhizoblum group; Bradyrhizobium.
ACBI_TaxID=375;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; U12678; AAC28892.1; -. HSSP; P08074; 1CYD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Tully R.E., van Berkum P., Lovins K.W., Keister D.L.;
"Identification and sequencing of a cytochrome P450 gene cluster
Bradyrhizobium japonicum.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          "Cloning and mutagenesis of a cytochrome P-450 locus from Bradyrhizobium japonicum that is expressed anaerobically and symblotically.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
STRAIN-USDA 110;
Tully R.E., Keister D.L.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Biochim. Biophys. Acta 1398:243-255(1998).
-I- SIMILARITY: BELONGS TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Q45219;
01-NOV-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDLINE-98322110; PubMed-9655913;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Appl. Environ. Microbiol. 59:4136-4142(1993).
180
                                                       184
                                                                                                               120
                                                                                                                                                                    125
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ypothetical protein; Oxidoreductase.
                                                                                                                                                                                                                        64
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Local Similarity
                                                                                                                                                                                                                                                                                5
                                                                                                                                                                                                                                                                                                                                        Q
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                                                 HGVSCVSLWPGIVQTELLK - - EHMAKEEVL
                                                                                                                                                                                                                                                                                                                            GKVAVVTGAGAGIGKACALAIAREGGRVVVA--DIDGSAAIACTAQIAAEAGHALAIAID
                                                                                                                                                                                                                                                                                                                                                                                       GQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQEAQ--SLGGQCVPVVCD
AQIRCNAVAPGLIMTERLRMQTHLRRHQLL
                                                                                                         RGTLLCCRQAIPRMIARGGGAIVNMSSCQGLSGDTALTSYAASKAAMNMLSSSLATQYGH 179
                                                                                                                                                           RGHYFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCAHELRR 183
                                                                                                                                                                                                                  IADAQAVAALFETAER-HFGGVDLLVNNASA---MHLTPRDRAILELELAVWDQTMARNL
                                                                                                                                                                                                                                                                       SSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGL
                                                                                                                                                                                                                                                                                                                                                                                                                                                 65;
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159
275 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Conservative
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2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28827 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                              34;
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Pred. No. 1.7
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                                                                                                                                                                                                                                                                                                                                                                                                                                              100;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SIMILARITY).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length 275;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                              11;
                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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RESULT 12 Y019\_THEMA

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Melson K.E., Clayton R.A., Gill S.R., Gwinn M.L., Dodson R.J.,

Haft D.H., Hickey E.K., Peterson J.D., Nelson W.C., Ketchum K.A.,

McDonald L., Utterback T.R., Malek J.A., Linher K.D., Garrett M.M.,

Stewart A.M., Cotton M.D., Pratt M.S., Phillips C.A., Richardson D.,

Heidelberg J., Sutton G.G., Fleischmann R.D., Eisen J.A., White O.,

Salzberg S.L., Smith H.O., Venter J.C., Fraser C.M.;

"Evidence for lateral gene transfer between Archaea and Bacteria from.

genome sequence of Thermotoga maritima.";

Nature 399:323-329(1999).

Nature 399:323-329(1999).
                                                                                                                                                                                                                            ACT_SITE CONFLICT SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Ew the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content
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Q56318;
                                                                                                                                                                                                                                                                                                                                                               EMBL; X85171; CAA59459.1; -. EMBL; AE001690; AAD35113.1; HSSP; P19992; 1HDC.
                                                                                                                                                                                                                                                                                                                                                                                                                                 modified and this statement entities requires a license
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Molecular and phylogenetic characterization of pyruvate and 2-
keto1sovalerate ferredoxin oxidoreductases from Pyrococcus furiosu
and pyruvate ferredoxin oxidoreductase from Thermotoga maritima.";
J. Bacteriol. 178:248-257(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                      or send
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 STRAIN-MSB8 / DSM 3109;
MEDLINE-96125254; PubMe
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Bacteria;
                                                                                                                                                                                                                                                                                                             PRINTS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRAIN=MSB8 / DSM
MEDLINE=99287316;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Thermotoga maritima.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-MAY-2000
16-OCT-2001
                                                                                                                                                                                                                                                                                  Hypothetical
                                                                                                                                                                                                                                                                                                PROSITE;
                                                                                                                                                                                                                                                                                                                         Pfam; PF00106; adh
                                                                                                                                                                                                                                                                                                                                                     TIGR;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Kletzin A., Adams M.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-NOV-1997
                       123 GLRGHYFCSVYGARLMVPAGQGLIVVISSPGSLQYMFNV-PYGVGKAACDKLAADCAHEL
                                                     60
                                                                              63
                                                                                                                                                                          Local
                                                                                                                                                                                                                                                                     BIND
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (SDR) FAMILY.
                                                                  CDSSQESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASKMDDINNV | : | : : | | : : | : : | : : |
NLTGPYICSRYCAEEMIKRGGGVIINIASTRAFQSEPDTEPYSASKGGLVALTHSLAVSL
                                                 TOVADENSVKNMYRKT-VEIXGGVDVLVNN--AAVMSV-----KSIFERPLEEWERVIRV
                                                                                                      LEGKVAVVTGGGQGIGAAIAQLFAENGMKVVIA--EIDEEAGVEREEMLRERGLDVTF'VK
                                                                                                                                 MNGQVCVVTGASRGIGRGIALQLCKAGATVYITGRHLDTLRVVAQE--AQSLGGQCVPVV
                                                                                                                                                                                                                                                                                                                                                   TM0019;
                                                                                                                                                                                                                                               Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                     an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                       IPR002198; ADH_short.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermotogales;
                                                                                                                                                                                                                            153
130
256 AA;
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(Rel.
                                                                                                                                                             Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  35, Greated)
39, Last sequence update)
40, Last annotation update)
uctase TM0019 (EC 1.-.--).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3109;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PubMed-8550425;
                                                                                                                                                                                                                                           33
153
136
                                                                                                                                                                                                                                                                                                                                                                                                                               latement is not removed. Usage by and for commercial license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                                                                                                                               28078 MW;
                                                                                                                                                                       12.9%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Thermotoga
                                                                                                                                                             41;
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BY SIMILARITY.
RGGGVII -> TRWRSDH (
W; D68160B1D7980C6B (
                                                                                                                                                                          Pred.
                                                                                                                                                                          Score 209; DB 1;
Pred. No. 3.6e-10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
                                                                                                                                                             Mismatches
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furiosus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          a collaboration
-
MBL outstation
                                                                                                                                                            Gaps
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 171
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RESULT 13
FABG_ARATH
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     ACT_SITE
SEQUENCE
                                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the EM the European Bioinformatics Institute. There are no restruse by non-profit institutions as long as its content modified and this statement is not removed. Usage by and entitles requires a license agreement (See http://www.isb-s
                                                                                                                                                                                                                                                                                                                                                                                                                                 -!- CATALYTIC ACTIVITY: (3R)-3-hydroxyacyl-[acyl-carrier protein]
NADP(+) - 3-oxoacyl-[acyl-carrier protein] + NADPH.
-!- PATHWAY: FIRST REDUCTION STEP IN THE FATTY ACID BIOSYNTHESIS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         01-FEB-1994 (Rel. 28, Created)
01-FEB-1994 (Rel. 28, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
3-oxoacyl-[acyl-carrier protein] reductase, chlocker (EC 1.1.100) (3-ketoacyl-acyl carrier protein Arabidopsis thallana (Mouse-ear Cress)
                                                                                                PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
Fatty acid biosynthesis; Oxidoreductase; NADP;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "Molecular cloning of higher-plant 3-oxoacyl-(acyl carrier protein) reductase. Sequence identities with the nodG-gene product of the nitrogen-fixing soil bacterium Rhizobium meliloti.";
Biochem. J. 283:321-326(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MEDLINE=92246853; PubMed=1575676; Slabas A.R., Chase D., Nishida I., Murata N., Sidebottom C., Safford R., Sheldon P.S., Kekwick R.G.O., Hardie D.G.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                CHAIN
                                                                                                                                                                                                                                  or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBUNIT: HOMOTETRAMER (PROBABLE).
-i- SUBCELLULAR LOCATION: CHLOROPLAST AND NON-PHOTOSYNTHETIC
                                                                                                                                                                                       PIR; S22416; S22416.
                                                                                                                                                                                                         EMBL; X64464; CAA45794.1; -.
                                                                                                                                             interPro; IPR002198; ADH_short.
                                                                                                                                                                              ISSP; P50162; 1AE1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mackintosh R.W.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=3702;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           182
                                                                                                                                                                                                                                                                                                                                                                  SIMILARITY: BELONGS TO
                                                                                                                                                                                                                                                                                                                                                      (SDR) FAMILY.
                                                                                                                                                                                                                                                                                                                                                                                                                           PATHWAY.
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                                                                                       peptide.
 81
226
319
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105
226
33621
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    ₩;
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                 NADP (BY SIMILARITY).
BY SIMILARITY.
                                               REDUCTASE.
                                                        CHLOROPLAST (BY SIMILARITY).
3-OXOACYL-[ACYL-CARRIER PROTEIN]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRT;
  BE3D8304023EBFCF CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                319
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                                                                                                Chloroplast;
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                                                                                                                                                                                                                                                                                                     EMBL outstation
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Query Match 12.7 Best Local Similarity 24.9 Matches 70; Conservative

12.78;

49;

Score 206; DB 1; Pred. No. 8.3e-10; 9; Mismatches 110

110;

52;

Gaps

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Query Match Best Local S Matches '61

1 Similarity 61; Conserv

12.6%; nilarity 26.9%; Conservative 4

40;

Mismatches

116;

;0

Gaps

4

Score 204; DB 1; Pred. No. 9.5e-10;

Length Indels

262;

Length 319 Indels

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           RESULT
                                                                                                                                                                                                                                                                                                                                                                                                                                          Hypothetical oxidoreduct, YXBG OR E3BR. Bacillus subtilis. Bacteria; Firmicutes; Bac Bactllus/Staphylococcus;
    Hypothetical | NP_BIND | ACT_SITE | 1: SEQUENCE | 26:
                                                  Pfam; PF00106; adh_short; 1.
PRINTS; PR00080; SDRFAMILY.
PROSITE; PS00061; ADH_SHORT; 1.
                                                                                                                       EMBL; AB005554; BAA21601.1; -. EMBL; Z99124; CAB16020.1; -. HSSP; P25529; IFMC.
                                                                                                                                                                                                                                                                                                                "Cloning and sequencing of a 36-kb region of the Bacillus genome between the gnt and iol operons.";
DNA Res. 2:61-69(1995).
                                                                                             SubtiList; BG11357; yxbG
InterPro; IPR002198; ADH
                                                                                                                                                                         or send an email to license@isb-sib.ch).
                                                                                                                                                                                       use by non-profit institutions as long as its content modified and this statement is not removed. Usage by an entities requires a license agreement (See http://www.isb-
                                                                                                                                                                                                                         This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Enthe European Bioinformatics Institute. There are no restricted the European Bioinformatics Institute.
                                                                                                                                                                                                                                                                            -1- SIMILARITY: TO E.COLI 7-ALPHA-HYDROXYSTEROID DEHYDROGENASE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1995
16-OCT-2001
                                                                                                                                                                                                                                                                                                            -1- SIMILARITY: BELONGS
                                                                                                                                                                                                                                                                                                                                                                                           STRAIN-
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P46331;
                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       01-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             270 DMEKKILGTIPLGRYGKAEEVAG--LVEFLALSPAASYITG
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                                                                                                                                                                                                                                                                                               (SDR) FAMILY.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SCVSLWPGIVQTELLKEHMAKEEVLQDPVLKQFKSAFSSAETTELSGKCVVALATDPNIL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            YFCSVYGARLMVPAGQGLIVVISS-PGSLQYMFNVPYGVGKAACDKLAADCAHELRRHGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ATDVDAMMKTA-LDKWGTIDVVVNN--AGI----TRDTLLIRMKQSQWDEVIALNLTGV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ESEVRTLFEQVDREQQGRLDVLVNNAYAGVQTILNTRNKAFWETPASMWDDINNVGLRGH
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                                                                                                                                                                                                                                                                                                                                                                                           168
    155
262 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (Rel. 32, Created)
(Rel. 32, Last sequence update)
(Rel. 40, Last annotation updat
coxidoreductase yxbG (EC 1.-.-.
                                          protein;
                                                                                                                                                                                                                                                                                                                                                                                         BGSC1A1;
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  155 E
28232 MW;
Oxidoreductase; NAD; Complete proteome.
NAD (BY SIMILARITY)
S BY SIMILARITY
15 BY SIMILARITY
18232 MW; A7EE37514F07EDF4 CRC64;
                                                                                              ADH_short.
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                                                                                                                                                                                                                                                                                                      TO THE SHORT-CHAIN DEHYDROGENASES/REDUCTASES
                                                                                                                                                                                                                                                                                                                                                                                                                                           group;
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SEQUENCE FROM N.A.
STRAIN-0157:H7 / EDL933 / ATCC 700927;
MEDLINE-21074935; PubMed-11206551;
Perna N.T., Plubkett G. III, Burland V., Mau B., Glasner J.D.,
Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,
Posfal G., Hackett J., Klink S., Boutin A., Shao Y.; Miller L.,
Posfal G., Davis N.W., Lim A., Dimalanta E.T., Potamousis K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-MAY 1992 (Rel. 22, Created)
01-MAY 1992 (Rel. 22, Last sequence update)
16-OCT-2001 (Rel. 40, Last annotation update)
7-alpha-hydroxysteroid dehydrogenase (EC 1.1.
HDHA OR HSDH OR B1619 OR Z2624 OR ECS2327.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HDHA_ECOLI
P25529;
                                                                                                            *A 570-kb DNA sequence of the Escherichia corresponding to the 28.0-40.1 min region DNA Res. 3:363-377(1996).
                                                                                                                                             "A 570-kb
                                                                                                                                                     Itoh T., Kasai H., Kashimoto K., Kimura S., Kitakawa M. Kitagawa M., Makino K., Miki T., Mizobuchi K., Mori H. Motomura K., Nakade S., Nakamura Y., Nashimoto H., Nis Oshima T., Saito N., Sampei G., Seki Y., Sivasundaram Tagami H., Takeda J., Takemoto K., Takeuchi Y., Wada C Yamamoto Y., Horiuchi T.;
                                                                                                                                                                                                                                       Alba
                                                                                                                                                                                                                                                                                                                                                          MEDLINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A.,
Riley M., Collado-Vides J., Glasner J.D., R
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Escherichia coli, and Escherichia coli 0157:H7.
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Mau B., Sh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-HB10
                                                                                                                                                                                                                                                    MEDLINE-97251357;
                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                         expressed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    gene from
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Yoshimoto T., Higashi
Kurazono K., Tsuru D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MEDLINE=91177803; PubMed=2007545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Escherichia
                                                                                                                                                                                                                                                                                                          Science
                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Cloning and sequencing of the 7 gene from Escherichia coli HB101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NCBI_TaxID=562, 83334;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Bacteria; Proteobacteria;
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"Crystal structures of the binary
hydroxysteroid dehydrogenase from
Biochemistry 35:7715-7730(1996).
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Hayashi T., Makino K., Ohnishi M., Kurokawa K.,
Han C.-G., Ohtsubo E., Nakayama K., Murata T., T
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Welch R.A., Blatt
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           FUNCTION: 7-ALPHA-BEHYDROXYLATION OF CHOLIC ACID, YIELDING DEOXYCHOLIC ACID AND LITHOCHOLIC ACID, RESPECTIVELY. HIGHEST AFFINITY WITH TAUROCHENODEOXYCHOLIC ACID.
CATALYTIC ACTIVITY: 3-alpha,7-alpha,12-alpha-trihydroxy-5-beta-cholanate + NAD(+) = 3-alpha,12-alpha-dlhydroxy-7-oxo-5-beta-cholanate + NADH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     SUBUNIT: HOMOTETRAME SIMILARITY: BELONGS
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JT0951; JT0951
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D90805; BAA15370.1;
D90806; BAA15377.1;
D90808; BAA15407.1;
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                                                                                                          PR00081; GDHRDH; PS00061; ADH_SI
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an email to license@isb-sib.ch)
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| Score<br>Pred.           |  | 49<br>PF-0475<br>N:   | , ve   | 14 G   | ALIG       | US-08-47-<br>PCT-US95-<br>US-08-25-<br>US-08-25-<br>US-08-25-<br>US-08-25-<br>US-08-25-<br>US-08-25-<br>US-08-25-<br>US-08-25-<br>US-08-83-<br>US-08-83-<br>PCT-US95-<br>PCT-US95-<br>US-08-84-<br>PCT-US95-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-<br>US-08-84-  |
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                                            IMMEDIATE SOURCE:
                                                                                                                      SEQUENCE CHARACTERISTICS:
                                                                                                                                                                           NAME: Billings, Lucy J. REGISTRATION NUMBER: 36,749 REFERENCE/DOCKET NUMBER: PFTELECOMMUNICATION INFORMATION: TELEPHONE: 650-855-0555
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MEDIAL: GELL
LIBRARY: GELL
CNR: 2315796
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ITLE OF INVENTION: HUMAN SHORT CHAIN DEHYDROGENASE
UMBER OF SEQUENCES: 3
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Matches 16
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INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
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SOFTWARE: Wordperfect (ASCII standard)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/375,962B
FILING DATE: 20-January-1995
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ADDRESSEE: Felfe & Lynch
STREET: 805 Third Avenue
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              12 VTGASRGIGR 21
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                                                                                                                                                                                                                                                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: LUD 5372.1 CIP
                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER:
                                                                                                                                                                                                                                  ENGTH:
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13, 1195
VTGASRGIGR 19
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16; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Application US/08375962B
                                                                                                                                                                                                                               244 amino acids
                                                   Conservative
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                                                                                                                                 E.coli 3-oxoacyl(acyl carrier protein)
reductase (FABG)
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                                                                                                                                                                                                                                                                                     688-9200
                                                                                                                                                                                                                                                                                                                                            Patricia A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Isolated Nucleic Acid Molecule Which Codes for A 32 kDa Protein Having 11-CIS Retinol Dehydrogenase Activity, and Which Associates With P63, a Portion of a Retinol Binding Protein Receptor
                                                                                                                                                                                                                                                                                                                                                                                     08/258,418
                                                                                                                                                                                                                                                                                                                            34,894
                                                             Score 10;
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Pred. No.
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US-08-562-114B-13 ; Sequence 13, Application US/08562114B

RESULT

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Patent No. 6280997
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Best Local
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TITLE OF INVENTION:
TITLE OF INVENTION:
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FILING DATE: 20-January-1995
ATTORNEY/AGENT INFORMATION:
NAME: Kohli, Vineet
REGISTRATION NUMBER: 37,003
REFERENCE/DOCKET NUMBER: LUD 5
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette, 3.5 inch, 144 kb storage
                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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                                                                                                                   STATE:
                                                                                                                                                                                         STREET:
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TLE OF INVENTION:
TLE OF INVENTION:
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                                                                                                                                         SEE: Felfe & Lynch
1: 805 Third Avenue
New York City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Application US/08729594A
                                                                                                                   New York
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Wordperfect 5.1 and ASCII
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838-3884
NO: 13:
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                                                                                                                                                                                                                                                                                                                                                         , Ulf; Simon, Andras; Romert, Anna
ISOLATED NUCLEIC ACID MOLECULE WHICH
CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL DEHYDROGENASI
ACTIVITY, AND WHICH ASSOCIATES WITH P63, A PORTION OF A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ISOLATED NUCLEIC ACID MOLECULE WHICH CODES FOR A 32 KDA PROTEIN HAVING 11-CIS RETINOL HYROGENASE ACTIVITY, AND WHICH ASSOCIATES WITH P63, A
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                                                                                                                                                                                                                                                                                                                               RETINOL BINDING PROTEIN
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NUMBER OF SEQ ID NOS: 2
SOFTWARE: FASTSEQ for Windows Vers
SEQ ID NO 2
LENGTH: 246
TYPE: PRT
ORGANISM: Staphylococcus aureus
US-09-238-481-2
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; NAME/KEY:
US-08-729-594A-13
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                                                           Query Match
Best Local Similarity
Matches 10; Conserv
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Best Local Similarity
Matches 10; Conser
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                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/238,481
CURRENT FILING DATE: 1999-01-28
                                                                                                                                                                                                                                                                                FILE REFERENCE: GM10192
                                                                                                                                                                                                                                                                                            APPLICANT: Huang, Jianzhong
APPLICANT: McDevitt, Damien
TITLE OF INVENTION: FabG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 08/258,418
FILING DATE: 10-June-1994
ATTORNEY/AGENT INFORMATION:
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12 VTGASRGIGR 21
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9 VTGASRGIGR 18
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SOFTWARE: Wordper
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R: 30,946
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Pred. No.
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Best Local Similarity
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SEQUENCE CHARACTERISTICS:
LENGTH: 255 amino acids
                                                                       NPPLICANT: Treadway, Patti J
                                                                                                      PPLICANT: Broughton, Mary C
PPLICANT: Crawford, Kathryn P
PPLICANT: Maddur1, Kishnamurthy
                                                                                                                                                PPLICANT: Baltz, Richard H
PPLICANT: Broughton, Mary (
RRENT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ELECOMMUNICATION INFORMATION: TELEPHONE: (317)337-4816
                                                                                                                                                                                                                                                                                                                             84 GRLDVLVNNA 93
                                                                                                                                                                                                                                                                                              94 GRLDVLVNNA 103
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DLECULE TYPE: protein
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: FILING DATE: 09-MAI
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Indianapolis
                                                                                                                                                                            INFORMATION:
   I: Waldron, Clive
INVENTION: Biosynthetic Genes For Spinosyn Insecticide
ERENCE: 50489 DIV1
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Broughton, Mary C.
Crawford, Kathryn P.
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US-08-793-035-9
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                                                                                            INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           EARLIER APPLICATION NUMBER: US 09/36987
EARLIER FILING DATE: 1998-03-09
NUMBER OF SEQ ID NOS: 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 25
TYPE: PRT
                                                                           SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 tent No.
                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 713.787.1400
                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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                                                                                                                                                                       REGISTRATION NUMBER:
                                                                                                                                                       REFERENCE/DOCKET NUMBER: MOBT:132
                                                                                                                                                                                                           IOR APPLICATION NUMBER: GB90,
APPLICATION NUMBER: GB90,
TOTAL
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                                                                                                                                                                                                                                                                                                                                  FILING DATE:
                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: US/08/793,035
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les 10; Conserv
                                                                                                                                                                                                                                                                                                                                                                                             OPERATING SYSTEM:
                                                                                                                                                                                                                                                                PPLICATION NUMBER: GB 9. ILING DATE: 20-JUL-1994
                                                                                                                                                                                                                                                                                                                   ASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                            NT APPLICATION DATA:
                                          amino acid
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              linear
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                                                           amino acids
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Query Match
Best Local Similarity

3.2%;

Score 10; Pred. No.

DB 3; 0.098;

Length 315

Matches

10; Conservative

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Mismatches

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Indels

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APPLICANT:

Bringer-Meyer, Stephanie

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                                                    RESULT 11
US-08-594-808B-7
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US-08-793-035-10
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Best Local Similarity
Matches 10; Conserv
                         equence 7, Application US/08594808B
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APPLICATION NUMBER: GB 9414622.2
FILING DATE: 20-JUL-1994
PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE: 17-JUL-1995
ATTORNEY/AGENT INFORMATION:
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  APPLICANT:
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                                                                                                          76
                                                                                                                                                                                                                                                      TYPE: amino acid
STRANDEDNESS: sin
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                    11 VVTGASRGIG 20
                                                                                                                                                                                                                                                                                                                                                                                NAME: Kammerer, Patricia A. REGISTRATION NUMBER: 29,775
                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: GB95/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/793,035
FILING DATE: 28-JUL-1997
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                                                                                                         VVTGASRGIG 85
              INFORMATION:
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Klasen, Ralf
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Best Local Similarity
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US-08-762-129-5
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                                                                                                                                                                                                                                                                                                                                            Sequence 5, Application US/08762129 Patent No: 5756299
                                                                                                                                                                                                                                APPLICANT: Hillman, Jenux R. APPLICANT: Goli, Surya K. TITLE OF INVENTION: A NOVE NUMBER OF SEQUENCES: 5
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
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             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,129
FILING DATE: Herewith
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ATTORNEY/AGENT INFORMATION:
NAME: Myers, Jonathan E
REGISTRATION NUMBER: 26,
                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: PatentIn Release #1:0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/594,808B FILING DATE: 07-FEB-1995
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MEDIUM TYPE: Floppy disk
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                              COUNTRY: UZIP: 94304
                                                                                                                                                                                                             STREET:
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OPERATING SYSTEM: PC-DOS/MS-DOS
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ZIP: 10471-0900
CLASSIFICATION:
                                                                                                                                                                                               CITY:
                                                                                                                                                                                                                            ADDRESSEE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           E: The Firm of Karl F. Ross, 5676 Riverdale Ave.
                                                                                                                                                               USA
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                                                                                                                                                                                                                            Incyte Pharmaceuticals, Inc
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                                                                                                               Diskette
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MICROBIOLOGICAL METHOD OF MAKING
5-KETOGLUCONATE
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0; Mismatches
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RIOR APPLICATION DATA:

PPLICATION NUMBER:

REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF TORNEY/AGENT INFORMATION:

PF-0171 US

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                                           NFORMATION FOR SEQ ID NO:
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                                                             REFERENCE/DOCKET NUMBER: FEI
ELECOMMUNICATION INFORMATION:
TELEPHONE: 312-616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                           tent No.
                                                                                                                         CLASSIFICATION: 435
CTASSIFICATION: 435
TTORNEY/AGENT INFORMATION:
                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30
                                                                                                                                                                                                                      MEDIUM TYPE: Floppy
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SEQUENCE CHARACTERISTICS:
LENGTH: 277 amino acids
STRANDEDNESS
                                                                                                    NAME: Mueller, Lisa L. REGISTRATION NUMBER: 3
                                                                                                                                                                                             COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                       ENGTH:
                                                                                                                                                               APPLICATION NUMBER:
                                                                                                                                                                                                                                                              COUNTRY:
                                                                                                                                                                                                                                                                                                                                                           TLE OF INVENTION
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nes 8; Conserv
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180 N. Stetson, Suite
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                Query Match
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US-08-858-207A-270
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                                                                                                                                       NFORMATION FOR SEQ ID NO:
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Best Local
                                                                                                                   SEQUENCE CHARACTERISTICS
LENGTH: 186 amino acid
                                                                                                                                                                                                                                                                                                SOFTWARE: FastSEQ for Windows Version 2.0 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/858,207A
                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                         TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-4478
                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                  CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                            STRANDEDNESS:
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                                                                                     COPOLOGY:
                                                                                                                                                                                                                                                        APPLICATION NUMBER:
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                                                                                                                                                                                                REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                             NAME: Gimmi, Edward R
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                              CITY: King of Prussia STATE: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                382 EEVLQDPV 389
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    Similarity 7; Conserv
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6348328
                                                                                                                186 amino acids
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  Conservative
                                                                                                                                                              610-270-5090

    SmithKline Beecham Corporation
    Nedeland Road

                                                                                                                                                                                                                                                                                                                                                                                                     USA
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                                                                                                                                                                                                                                                                                                                                                 IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hodgson, John
Knowles, David
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Mismatches
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                  Length 186;
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US-09-239-052-2
; Sequence 2, Application US/09239052
; Patent No. 6346395
; GENERAL INFORMATION:
; APPLICANT: Homes, David J.
; APPLICANT: Bebouck, Christine
; APPLICANT: Bebouck, Christine
; APPLICANT: Debouck, Christine
; APPLICANT: Wang, Min
; APPLICANT: Wang, Min
; APPLICANT: Mosmarka, Anna L.
; APPLICANT: Chalker, Alison F.
; APPLICANT: Mosmarka, Anna L.
; APP
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